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					SUMMARIES		
Result No.	8	% Query Match	Length	DB	QI	scr	ion
-	1244.8	81.0	3124	י י י	AF311905	AF311905	Homo sapi
N	1100.4	71.6	2374	w	CQ842614	CQ842614	Sequence
ო	1100.4	71.6		σ	AK122619	AK122619	Homo sapi
4	1082	70.4		ø	AX365516	AX365516	Sequence
ιΩ	1078.8	70.2		9	CQ767791	CQ767791	Sequence
9	1078.8	70.2		ω	AX376050	AX376050	Sequence
7	1078.8	70.2		σι	AY358337	AY358337	Homo sapi
œ	956.2	62.3		ø	AX365530	AX365530	Sequence
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10	956.2	62.3		ω	AX365542	AX365542	Sequence
11	954.6	62.1	2176	σ	AF310233	AF310233	
12	869.2	56.6		9	AX497858	AX497858	Segue
13	787	51.2		ω	BD011516	BD011516	
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15	779	50.7		σ	AY032685	AY032685	Homo sapi
16	777.8	50.6		છ	AX365544	AX365544	Sequence
17	777.4	50.6	229	9	BD261703	BD261703	
18	740.8	48.2	2076	v	CQ733422	CQ733422	Sequence
19	738	48.0	2954	9	AX365517	AX365517	

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AF311905 3124 bp mRNA linear PRI 21-AUG-2001 Homo sapiens sialic acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds. AF311905 AF311905.1 GI:15217165	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Li,N., Zhang,W., Wan,T., Zhang,J., Chen,T., Yu,Y., Wang,J. and Cao,X. Cao,X. Cloning and characterization of Siglec_10, a novel sialic acid	Dindling member of the 1g superiamily, from numan dendritic cells J. Biol. Chem. 276 (30), 28106-28112 (2001) 11359381 11358961 2 (bases 1 to 3124) 12. (bases 1 to 3124) 13. (bases 1 to 3124) 14. (bases 1 to 3124) 14. (bases 1 to 3124) 15. (bases 1 to 3124) 16. (bases 1 to 3124) 17. (b	Direct Submitt Medica]	/mol_trype="mRNA" /db_xref="taxon:9606" 13124 /gene="SIGLECIO" 2232031	/gene="SIGLEC10" /note="Siglec-10; similar to other siglec family members" /codon_start=1 /codon_estart=1 /product="sialic acid-binding Ig-like lectin 10" /protein_id="AAK92542.1" /db xref="GI:15217166" /translation="MLPLLSSLGGSQAMDGRFWIRVQESWWVPEGLCISVPCSFS YPROPWYGSTPAYGYWFRAYTETTKGAPVATNHQSREWEMSTRGRFQLTGDPAKGNCS LVIRDAQMQDESQYFFRVERGSYVRYNFWNDGFFLKVTALIQKPDVXIPETLEPGQPV
RESULT 1 AF311905 LOCUS DEFINITION ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL FEATURES SOURCE	gene	

TDLTCHVD SQFLRLLC NRLGSQQR SPPARLSW HYKKGLLS DYINVVPT	
TVICVENWAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVD FSRKGVSVQRTVRLAVAYARPDLVISISRDWTPALEPQPQGNVPYLEAGAKGQFTKLLC ABOOPPATLISWVLQNRVLISSSHPWGPRPLGLELFGVYAGOSGRYTCRAENRIGSQQR ALDLSVQYPSENLI WWWSQANRTYLBNIGNGTSLPVLEGQSLGLVCTWFSSPPRRLSW TQRGQVLSPSQPSDPGVLELPRVQVBHZGEFTCHARHPLGSQLVSUSCUSVTHSSPPRLSW TAFSWGAFLGIGTTALLFLCLALI INKILPKRRTQTETPRPKFSRFRIJLDYINVVPT AGDLAQKTROKATPNSPRTILLSPGAPSPESKKNOKKQYQLPSFPRFKSSTQAPESQBS OBELHYATLNFPGYRSPREARMPKGYOADYARVKFO"	
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163 ACGGGGGTGCCTCTCCTCCCAAGGAACCAACGAACCAACTCTCCAATGCTC 822 883 AGAAAGGGTGTGAGGGTACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC 942 282 582 480 643 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCCAGCCGGTG 702 540 601 AGCTTCACGCCCAGACCCCAGGACCACGACCTCACCTGCCATGTGGACTTCTCC 660 AGCTTCACGCCCAGACCCCAGGACCACACCGACCTCACCTGCCATGTGGACTTCTCC 882 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC 720 GAGGIGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGGCCAAGGGGAAC 300 TGCTCCTTGGTGATCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG 403 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 463 GAGGTGGAAATGAGCACCCGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGAAC 223 Argeracidecaciderderecrecideridecidecedesiceadecrarganidada TICTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCCACAAACCACCAGGAGTCGA GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG Gaps Oper Match 81.0%; Score 1244.8; DB 9; Length 3124; BEGE Local Similarity 84.7%; Pred. No. 0; Marches 1529; Conservative 0; Mismatches 7; Indels 270; CTIGITATCAGCATTTCACGTGACACACGCCAG---------361 823 19 283 121 343 181 241 301 523 583 421 481 199 721 943 755 755

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SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Nammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.  REFERENCE AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.  TITLE Pull-length human cdna JOURNAL Patent: EP 1440981-A 1261 28-UUL-2004; Research Association for Biotechnology (JP) Location/Qualifiers Source //organism="Homo sapiens" /mol type="massigned DNA" /db_xref="taxon:9606"	Duery Match  Best Local Similarity 87.7%; Pred. No. 2.7e-285;  Best Local Similarity 87.7%; Pred. No. 2.7e-285;  Matches 1288; Conservative 0; Mismatches 6; Indels 174; Gaps 1;  69 ACGAGTGCAGGAGTCAGTGATGGTGCCGAGGGCTGTGCATCTGTGCCCTGCTTTT 128	489 CIGIGIGITITAACTGGGCCTTTGAGGAATGICCACCCCCTTCTTTCTCCTGGACGGGGGC 54 353

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                                               Kazusa Kamatari, Kisarari, Chiba 292-0818, Japan (Ermail:genomics@hri.co.jp, Tel:81-438-52-3876, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5. & 3.-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; All and RAB.

RAB; annotation: HRI and RAB.

Location/Qualifiers
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SNOAFLGITTALLFUCLALIMKILEKRRTQTDETPRRPRSRHSTILDVINVVPRAGP
IVOKRNQKATPSSPRTPLPPGAPSPSSKKNOKKGYQLPSFPEPKSSTQAPESQESQEE
LHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ"
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                                 (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
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/clone_lib="SpLEN2"
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                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="BAC85493.1"
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/clone="SPLEN2001599"
Isogai, T. and Yamamoto, J. Direct Submission Submitted (15-JUL-2003) T
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CTGGGAATCGGCATCACGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCATGAAGATT 1388 CTGGAAAACCTTGGGAACGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCTG ATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAG decigenadacterecedadecadaadeadecineeeneedadecadecadeceneeacene TCTGTGCAGTATCCTCCAGAGAACCTGAGAGGGATGGTTTCCCAAGCAAACAGGACAGTC CTGAGCCCTCCCAGCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGGGTTT CTACCGAAGAGGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACG AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCCAGAACCCAAATCATCCACT AAGAAGAACAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAAATCATCCACT CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA **GCCGTCAGACCCAGGCCTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGCAGAA** -----AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG CTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATT CAAGCCCCAGAATCCCAGGAGACCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA GTCTGTGTCACACACAGCCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGGACAGGTT GGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCC linear DNA 2764 bp I from Patent EP1386931. CQ767791 Seguence 258 from Pateni CQ767791 CQ767791,1 GI:45108134 Homo sapiens (human) Homo sapiens GICAAGIICCAA 1536 1509 1629 1689 606 1029 1089 1149 1045 1269 1329 1389 1225 1449 1285 849 696 805 1209 1105 1165 1345 1569 1405 1465 1525 1749 702 865 925 985 753 RESULT 5
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Novel siglecs and uses thereof
Patent: WO 202627-A 131-73N-2002;
BRISTOL-MYERS SQUIBB COMPANY (US)
Location/Qualifiers
1. 2565
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db\_xref="taxon:9606" 1 from Patent W00208257. Homo sapiens Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates, GI:18697085 70.4%; llarity 81.6%; Conservative C Homo sapiens (human) Sequence 1 f AX365516 AX365516.1 Ouery Match Best Local Similarity Matches 1331; Conserv 549 609 699 546 129 61 189 121 249 181 309 241 369 301 429 361 489 421 460 486 729 909 642 ACCESSION VERSION KEYWORDS SOURCE ORGANISM source DEFINITION REFERENCE AUTHORS TITLE JOURNAL PEATURES DRIGIN d ò D S ਨੇ ò

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Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                Ë.
                                             Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, Human neurotrimin homologue
Patent: BP 138691-A 258 04-FEB-2004;
Genentech, Inc. (US)
Location/Qualifiers
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                                                                                                                                            /organism="Homo sapiens"
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1 0/05 13051 1365 1464 1164 1665 1294 1545 1044 調 12,24 1125 1104 1605 1404 1344 1485 1425 1524 PAT 01-MAR-2002 945 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 985 CACGAAGGAGATTCACCTGCCACGCTCCGCACTGGGCTCCCAGCACGCTCTGTTTC CTGGAAAACCTTGGGAACGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGGCTG 1066 CTGAGCCCCTCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGGA 1126 CACGAAGGAGATTCACCTGCCACGCTCGGCACCTGGGCTCCCAGGCACGTCTGGTCT CTGGGAATCGCCATCACGCTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATT 1165 CTACCGAAGAGGACGGACTCAGACACAGAGGCCCCAGGTTCTCCCGGCACAGCACG 1306 CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGGACG 1225 ATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCTGGCTCAGAAGCGGAAAGCAG 1486 AAGAAGAACCAGAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATG©ACT 1606 GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAAA ---AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAACAGGAGAGTC 886 retgraceagrarecredagaacergagagracergargargerreccaageaacaggagae 946 credanancerrescandescarcererecentracesascerandescere GTCTGTCACACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAAA CTGAGCCCCTCCCAGCCCTCAGACCCCGGGTCCTGGAGCTGCCTCGGGTTCAAGAGGAG AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT 1186 AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGGGTTT 1246 CTGGGAATCGGCATCACGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCATGAAGATT 1285 AAAGCCACACCAAACAGICCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCA 1345 AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATGCACT 1405 CAAGCCCCCAGAATCCCAGGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1546 CAAGCCCCAGAATCCCAGGAGGAGCCAGGAGCTCCATTATGCCACGCTCAACTTCCCA GOCCICAGACCCAGGCCTGAGGCCCGGATGCCCCAAGGGCACCCCAGGCGGATTATGCAGAA linear DNA Seguence 117 from Patent WO0168848.

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2764)
Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Chen, J., Eston, D., Foster, J., Grimaldi, C., Guo, Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Kilmowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
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                                       Patent: WO 0168848-A 117 20-SEP-2001,
Genentech, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="unassigned DNA"
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Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale, Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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llarity 81.4%; Pred. No. 1.8e-279;
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Db 1546 CAAGCCCCAGAATCCCAGGAG	Qy 1465 GGCGTCAGACCCAGGCCTGAG	1525		AX365510 LOCUS LOCUS DEFINITION SEquence 15 from Patent AXCESSION AX365530 VERSION AX365530.1 GI:18697092	KEYWORDS . SOURCE Homo sapiens (human) ORGANISM Homo sapiens	Eukaryota; Metazoa; Mammalia; Eutheria;	AUTHORS Longphre, M., Chang, H. a. TITLE Novel siglecs and uses	BRISTOL-	source 12208 /organism="Homo sa: /mol_type="unassig	/db_xref="taxo	V Match 62.3%; Local Similarity 73.3%; hes 1533; Conservative	OY 1 AIGCIACIGCACIGCTG  Db 118 AIGCIACIACACIGCTACTG  TO THE TO TH	61 178	121 23 238	OY 181 TTCAAAGCAGTGACTGAGACA 	241		361	Db         478 GAGAGAAGCTATGTGAGAN           Qy         421 GCCCTGACTCAGAAGCCTGATC	538	OY 481 ACGGTCATCTGTGTGTTTAAC) Db 598 ACGGTCATCTGTGTGTTTAAC)

AF301007 AF301007.1 GI:21956185 Homo sapiens (human)

longphre, M., Whitney, G.S., Wang, S., Chang, H. and Yan, W.P. Direct Submission
Submitted (29-Aug-2000) Immunology Department, Bristol-Myers Squibb Pharmaceutical Research Institute, Route 206 and Province Line Road, Princeton, NJ 08543-4000, USA /codon\_start=1 /product="sialic acid-binding immunoglobin-like lectin 10" /protein\_id="ApM81254.1" /db\_xref="GI:21956186" /trānslation="MLLPLLLSSLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFS AF301007 3012 bp mRNA linear PRI 26-JUL-2002 Homo sapiens sialic acid-binding immunoglobin-like lectin 10 (SIGLECIO) mRNA, complete cds. cells of the CD33 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 3012)

Whitney(G.S., Wang,S., Chang,H., Cheng,K.-Y., Liu,P., Zhou,X.D., Yan,W.P. and Longpire,M.
A new Siglec family member, SIGLECIO, is expressed in cells of the immune system and has signaling properties similar to CD33 /organism="Homo sapiens" /mol type="mRNA" /db\_xref="taxon:9606" /chromosome="19" /map="19q13.33-q13.41" 1<u>1</u>8. .2211 /gene="SIGLEC10" gene="SIGLEC10" .3012 .3012

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AGACGGACTCAG 1185 AGACGGACTCAG 1868 CAGAAAASCAG 1365 |||||||||||| |CAGAAAASCAG 2048 CAAACAGRCCT 1305 CAAACAGRCCT 1988 HATCCCAGGAG 1425CM CCCAGGCCTGAG 1485 PRI 22-MAY-2001 TGCCAGATAAG 1748 ces, University nited Kingdom Euteleóstomi; er, P.R. ression of CAA 1536 ||| CAA 2219

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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Ramkumar,J., Lu,Y., Lo,T.P., Gururajan,R., Gandhi,A.R., Arvizu,C.
and Yao,M.G.
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/mol_type="unassigned DNA"
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/noce="Incyte ID No: 7701502CB1"
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Patent: WO 0240671-A 8 23-MAY-2002,
Incyte Genomics, Inc. (US)
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Sequence 8 from Patent WO0240671.
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Sikly, K.K. and Miller, C.L.E.

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PP 27-MAY-1999 UP 1999500864

PR 27-MAY-1997 US

FR 27-MAY-1997 US

FR 27-MAY-1997 US

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Sialoadhesin family 4(SAF-4) cDNA.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 3099)
1 (Klly, K. and Miller, C.L.E.
Sialoadhesin family 4 (SARF-4) CDNA
Patent. JP 201502359-A 2 20-FEB-2001;
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PN JP 20012359-A/2
PD 20-FEB-201359-A/2
PP 27-MAY-1998 JP 1999500864
PR 27-MAY-1997 US GO/047572
PI KRISTINE KAY KILLY CONNIE LYNN ERICKSON MILLER PC
AGIK38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705,
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/ Organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sialoadhesin family 4(SAF-4) cDNA.
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20-FBB-2001
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Matches 1331; Conservative 0
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Homo sapiens (human)
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                                                                                    GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
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Protein id="AAK51124.1"
/db xref="GI:20384702"
/translation="MLLPLLLSSLLGGSQAMDGRFWIRVQEPVMVPEGLCISVPCSFS
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                                                                                                  acid-binding protein splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                               50.7%; Score 779; DB 9; Length 2126;
llarity 69.2%; Pred. No. 1.2e-198;
Conservative 0; Mismatches 210; Indels 381;
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                               GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 1370
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[Dases 1 to 2126)

Kitzig.F., Martinez-Barriocanal, A., Lopez-Botet, M. and Sayos, J.

Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SiP-1

Biochem. Blophys. Res. Commun. 296, 355-362 (2002)

Kitzig.F., Alvarez-Errico, D., Sayos, J. and Lopez-Botet, M.

Direct Submission

Submitted (17-APR-2001) Immunology, Universitat Pompeu Fabra (CEXS), Dr. Alguader No. 80, Barcelona 080003, Spain
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/db_xref="taxon:9606"
/chromosome="19"
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TITLE
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AUTHORS
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817	GACAGCCAGCCCCTGCCACATTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC 876
642	CTGCCATGTGGACTTCTCCAGAAAGGTGTGAGCGCACAGAGGACGTCCGACTCCGTGT 701
702	GGCCTATGCCCCAGAGACCTTGTTATCAGCTGTGACAACAGGCC 752
753	AGATCCTCCAGAGAACCTGAGAGGTGATGGTTTCCCAAGGAAAGGGACAGTC 804
805 1057	CIGGAAAACCIIGGGAACGGCACGICICICCCAGIACIGGAGGCCAAAGCCIGIGCCIG 864
865	GTCTGTGTCACACACACCCCCCCAGCCTGAGCTGGACCCAGAGGGACAGGTT 924
925	CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGCAGCTGCCTCCGGGTTCAAGTGGAG 984
985	CACGAAGGAGTICACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC
1045	AGCCTCTCCGTGCACT1060
1061	10
1357	GGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGCCTCTCTGCGCTGGTGGCTT 1416
1061	1060
1417	GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 1476
1001	1060
1477	GCCGGGCCCTGGGCCAACAGCTCCCTGAGGCCTCCATGGAGGCCTCAGCTCCGGCCTCAGG 1536
1061	106
1537	CICCGCTGTGAGGCCTGGAACGTCCATGGGGCCCCAGAGTGGATCCATCC
1061	-ATAAGAAQGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTTCTGGGAATCGGCATC 1119 
1120	ACGGCTCTTCTTTTCCTCTGCCCTGATCATCATGAAGATTCTACCGAAGAGAGGG 1179
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1240	AATGTGGTCCCGACGGCTGGCTCGGCTCGGAAGCGGAATCAGAAAGCCACACCAAC 1299
1300	AGECCEGGACCCCTCTECACCAGGTGCTCCCTCCCCAGAATCAAAGAACCAGAAA 1359 
1360 1897	AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1419 
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1420 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1479	1957 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACGCAGG 2016	1480 CCTGAGGCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCAA 1536	2017 CCTGAGGCCCGGATGCCTAAGGCGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 2073	Search completed: November 8, 2004, 16:01:43 Job time : 10392.4 secs
1420	1957	1480	2017	complet ne : 103
ò	g G	ò	qq	Search Job tin

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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8, 2004, 05:07:09; Search time 1055.14 Seconds (without alignments) 7641.758 Million cell updates/sec 1 atgotactgocactgotgot......atgoagaagtoaagttooaa 1536 using sw model US-09-937-636-1 1536 OM nucleic - nucleic search, November Title: Perfect score: Sequence: Run on:

IDENTITY NUC Gapext 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2002bs;\* geneseqn2003as;\* geneseqn2003bs;\* geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* N Geneseq 23Sep04:\* geneseqn1980s:\* geneseqn1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Aaa37847 Human obe	Abk43360 DNA encod	Aaz34109 Human PRO	Aac78510 Human PRO	Aas45983 Human DNA	Aca63677 Novel hum	Aca89433 cDNA enco	m	Aca05758 Human sec	Aca66592 cDNA enco	Acf20167 Human sec	Acf19553 Human sec	Acd21841 Human sec	Acf13006 Human sec	Acd25109 Human sec	Acf00158 Human sec	Aca72215 Novel hum	Acd04739 Novel hum	Acd18200 Human sec	Acd08207 Human sec	Aca88641 Novel hum
	Π	AAA37847	ABK43360	AAZ34109	AAC78510	AAS45983	ACA63677	ACA89433	ACA73443	ACA05758	ACA66592	ACF20167	ACF19553	ACD21841	ACF13006	ACD25109	ACF00158	ACA72215	ACD04739	ACD18200	ACD08207	ACA88641
	DB	ო	9	N	m	4	œ	œ	ω	ω	œ	ω	ω	ထ	ω	ω	œ	∞	œ	œ	œ	8
	Query Match Length DB	1536	2565	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	76	76	2764	76	76
æ	Query	100.0	70.4	70.2	70.2	70.2	70.2	70.2	О	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2	70.2
	Score	1536	1082	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8
	Result No.	ן ר	7	m	4	ς,	9	7	60	o	10	11	12	13	14	15	16	17	18	19	20	21

Aca70083 Human sec	Acd12305 Novel hum	Acc74220 Human sec	8 Human	Acd25416 Novel hum	Acd17893 Human sec	Acc88180 Human sec	4	Acd18601 Human sec	Aca71841 Human sec	Abx98211 Human cDN	Acd13962 Human PRO	Acd09742 Human sec	Acc88487 Human sec	Acd21227 Human sec		Abx92481 cDNA enco	Abx97802 Human PRO	Aca97278 Novel hum	Aca57741 Human PRO	Acd14269 Human PRO	Acc91052 Human sec	4 Human	Acd06991 Human PRO
8 ACA70083	8 ACD12305	8 ACC74220	8 ACD15848	8 ACD25416	8 ACD17893	8 ACC88180		8 ACD18601			8 ACD13962			8 ACD21227	8 ABX75599	8 ABX92481	8 ABX97802	8 ACA97278	8 ACA57741	8 ACD14269	8 ACC91052	4	8 ACD06991
2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764	2764
70.2	70.2	O	0	0	70.2	0	0	70.2	0	0	70.2	0	70.2	0	0	O	70.2	0		70.2			70.2
1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8		1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8	1078.8		٠.	1078.8	1078.8
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity, related disorder; therapy; ds. Human obesity protein binding protein-2 homologue coding sequence #1. AAA37847 standard; DNA; 1536 BP. (first entry) Homo sapiens. 12-FEB-2001 AAA37847; RESULT 1 AAA37847 

/\*tag= a /product= "hOB-BP2h" Location/Qualifiers 1. .1536 WO200059942-A2 Key

99US-0127667P. 22-MAR-2000; 2000WO-US006682. (ELIL ) LILLY & CO ELI. 02-APR-1999; 12-OCT-2000.

WPI; 2000-664992/64. P-PSDB; AAY97542. Wei J; Su EW,

New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders.

Claim 3; Page 85; 92pp; English.

This sequence encodes a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of

ö 540 120 240 240 360 420 480 540 999 720 780 840 120 180 180 300 300 360 420 480 009 900 099 720 780 09 09 Graphesity and/or obesity-related disorders. The hos-BP2h nucleic acids an useful as probes or amplification primers in the detection, agmantification or isolation of gene sequences or transcripts, for preparation and screening of antibodies, and in sense or antisense of suppression of hos-BP2h polypeptides, as immunogens in the suppression and screening of antibodies, and in sense or antisense of suppression of one or more hos-BP2h genes or nucleic acids, host cell of suppression of one or more hos-BP2h genes or nucleic acids, host cell of molypeptides are useful for raising or screening antibodies that the polypeptides are useful for raising or screening antibodies that sell of Sequence 1536 BP; 354 A; 487 C; 401 G; 294 T; 0 U; 0 Other; TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCCACAAACCACAGAGTCGA 301 iderectridergaleagaegeegeagargeagargagreacagargerg GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG 541 Acededecrecererectedadeaacaaacaaacaacacacacacarrectagaecre AGCTTCACGCCCAGACCCCAGGACCACGACCTCACCTGCCATGTGGACTTCTCC 661 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC 661 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC CTTGTTATCAGCATTTCACGTGACAACACGCCAGATCCTCCAGAGAACCTGAGAGTGATG criginalicadearinicaceneaeaeaeeeeeaareereeaeaeaeereaeaeere 781 GITICCCAAGCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGIA GTTTCCCAAGCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCCCAGTA 1 Argeracreceaeriderigerererederigesesesesereeerarigearideariga TGCTCTTTCTCCTACCCCCGACAGGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGGCCAAGGGGAAC TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG <u>ACGGTCATCTGTGTTTTAACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTCTCCTGG</u> AGCTTCACGCCCAGACCCCAGGACCACGACCACGACCTCACCCTGCCATGTGGACTTCTCC TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC TTCAAAGCAGTGACTGAGACAAGCGTGCTCCTGTGGCCACAAACCACCAGAGTCGA ACGGGGGCTGCCCTCCTCCCAAGGAACCAAACCAACGACCTCCCACTTCTCAGTGCTC Gaps ó; 100.0%; Score 1536; DB 3; Length 1536; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0; Onery Match Best Local Similarity 100. Malches 1536; Conservative 481 121 181 181 301 241 361 61 361 421 421 541 601 601 721 721 781

1260 1200 1380 1500 12007 1440 1260 1440 1500 1140 1140 1320 1380 1080 1320 1020 CTGGGCTCCCAGCACGTCTCTCTCTCCGTGCACTATAAGAAGGGACTCATCA CTGGGCTCCCAGCACGTCTCTCTCAGCCTCTCCGTGCACTATAAGAAGGACTCATCTCA ACGCATTCTCCAATGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTTCCTCTGC CATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAG 1441 CATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTCAGGCCCGGATGCGAAG GAGCTGCCTCGGGTTCAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCA gaderecercegerreaagregaecaceaagagagagrreaereceaecereceae Acescarrercaaresacerrreresaarescareacererererererere CCCAGGITCICCCGGCACAGCACCATCTGCATTACATCTAATGTCCTCCCGACGGTGGC CCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAACAGTCCTCGGACCCCTCTTCCA CCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAAAGCAGTATCAGTTGCCCAGT ccassingcrecerecessaricaassassascessaaaaseseerareserrecesser TTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTC GGCACCCAGGCGGATTATGCAGAGTCAAGTTCCAA 1536 1501 GGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1536 AGCTGGACCCAGAGGGGACAGGTTCTGAGCCCCT 196 1021 1081 1081 1141 1141 1201 1261 1261 1321 1321 1381 1381 1441 1501 901 901 1021 1201 961 RESULT 2 ABK43360 ð qq ð g ò g õ Ωp δ g δ QQ ò g ò g à g ð g ö qq

ВP ABK43360 standard; cDNA; 2565 (first entry) 05-JUN-2002 ABK43360

A 6 8

DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3a Human, sialic acid-binding Ig-related lectin, SIGLEC, asthma; mimune system disease, leuksemia, allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoathiritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis; gene, 8s.

WO200208257-A2 Homo sapiens 

20-JUL-2001; 2001WO-US023082 21-JUL-2000; 2000US-0220139P us-09-937-636-1.rng

m

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The invention relates to an isolated SIGLEC (sialic acid-binding Igralated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune bystem diseases such as asthma, leuksemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, following in the protein of the
                                                                                                                                                                                                                                 Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 2A; 209pp; English
   8
BRISTOL-MYERS SQUIBB
                                                                 Chang H,
                                                                                                                                   WPI; 2002-241565/29.
P-PSDB; AAU87074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
                                                                 Longphre M,
(BRIM )
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Sequence 2565 BP; 627 A; 765 C; 656 G; 517 T; 0 U; 0 Other;

240 Arecracreccacrecrecrecrecrecrecresecresereceaecraresaresares 120 248 180 308 368 300 GAGGIGGAAATGAGCACCCGGGCCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 428 360 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGAGATCTCTTCGGGTG 488 Gracificacerroaciceasaceceasecaseases en esta en consecuence en en esta en en en esta en en en esta en en entre en en entre entre entre en entre TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC TGCTCTTTCTCCTACCCCCGACAGGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA GAGGTGGAAATGAGCACCCGGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA Gaps 96; Length 2565; Indels Score 1082; DB 6; Pred. No. 1.2e-291; O; Mismatches 205; Query Match
Best Local Similarity 81.6%;
Matches 1331; Conservative 61 189 249 129 121 181 309 241 369 301 429 361 489 421 549 S S g g 8 8 장 염 8 Q ò 셤  $\delta$ 8 셤 8

1148 1044 1268 1328 1388 1448 1284 1464 1028 1088 1208 1104 1164 1224 1508 1568 1404 485 641 701 908 752 864 924 984 609 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCCTATGCCCCC AGAGACCTTGTTATCAGCATTTCACGTGACAACACGCCCAGCCCTGGAGCCCCAGCCCCAG **GGCTGCCCTCTCCTCCCAAGGAACCAAACCAACGACCTCCCCACTTCTCAGTGCTCAGCTT** ---GACACCGACCTCAC GACAGCCACCCCACACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC CTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT CATCCCTGGGGGCCCTAGACCCCTGGGGCTGCAGCTGCCCGGGGGTGAAGGCTGGGGATTCA <u> GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCTGGACCTTC</u> rcrerecagrariccrecagadaaccreagagrearegrinicecaageaaacaggacagre CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAAGCCTGTGCCTG GTCTGTGTCACACACACAGCCCCCAGCCAGCCTGAGCTGGACCCAGAGGGGACAGGTT CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG CACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGGCTCCCAGCACGTCTCTCT cacgaagaagagtrcaccrgccacgcrccacccacraggcrcccagcacgrcrcrc **AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTT** CTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATT CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACACAGG ATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAG Arcerddarracarcaargreereeeaceeeceeeceereeereaaaaceaaarcae **AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAAATCATCTT** AAGAAGAACCAGAAAAAAGCAGTATCAGTTGCCCAGTTTCCCCAGAACCCAAATCATCCACT CAAGCCCCAGAATCCCAGGAGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA CAAGCCCCAGAATCCCAGGAGGAGCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA GGAAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTGTGCTGCT -----AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT GGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCC CACGCCCAGACCCCAGGACCAC-----805 1029 1209 1045 1269 1389 1225 1449 1509 1345 789 849 702 753 696 1089 1149 985 1105 1329 1165 1285 1405 486 546 729 909 642 606 865 925 1569 ద 8 8 õ g ò g ò g ò d 8 셤 8 셤 Ś a ò 엄  $\dot{\delta}$ ద Š g  $\dot{\varsigma}$ g 8 음  $\dot{\delta}$ 임 ò 셤 ò 엄  $\stackrel{\diamond}{\circ}$ 셤

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The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ4438, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;
                                             28-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
                                                                                                                                               29-APR-1998;
29-APR-1998;
30-APR-1998;
                                                                                                                                                                                                06-MAY-1998;
06-MAY-1998;
07-MAY-1998;
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07-MAY-1998;
07-MAY-1998;
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13-MAY-1998;
13-MAY-1998;
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15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                    05-MAY-1998;
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15-MAY-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-
1465 GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA 1524
              1689 GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGCACCCCAGGCGGATTATGCAGAA 1748
                                                                                                                                                                                                                                     Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                                                                                                                                DE Human PRO940 nucleotide sequence
                                                                                                                                     AMZ34109 standard; cDNA; 2764 BP
                                                                                                                                                                                                                                                                                                                                                                                      98US-0077612P.
98US-0077612P.
98US-0077612P.
98US-0077711P.
98US-00740220.
98US-0078816P.
98US-00788239P.
98US-00788239P.
98US-00788239P.
98US-00788239P.
98US-0078624P.
98US-0079664P.
98US-0079664P.
98US-0079664P.
98US-0079668P.
98US-0079668P.
98US-007968P.
98US-0080121P.
98US-00801338P.
98US-0080134P.
                                                                        1749 Grcaagrrccaa 1760
                                                  1525 GTCAAGTTCCAA 1536
                                                                                                                                                                                       07-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                             NO9946281-A2.
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27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
30-MAR-1998;
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31-MAR-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1998;
21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                         16-SEP-1999
                                                                                                                                                                AAZ34109;
                                                                                                            RESULT 3
AAZ34109
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22-APR-1998

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New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.
                                                                                                                                                                                                                                                                                                                                                       Chen J;
                                                                                                                                                                                                                                                                                                                                                       Baker KP,
                                                                                                                                                                                                                                                                                                                                                       Gurney A, Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 92; 530pp; English.
98US-0086392P.
98US-0086414P.
98US-0086430P.
98US-0087698P.
98US-0087106P.
                                                                                                                                                                                                                                                                                                             98US-0087208P
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                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                       Wood WI, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551358/46.
P-PSDB; AAY41724.
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1185

1164

1224 1365 1284

1125

1425 1344 1485 1464

1605 1524 1665

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CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG
                                                                                                                                                                                                                                                                           CTACCGAAGAGAGGGACTCAGACAGAAACCCCGAGGCCCAGGTCTCCCGGCACAGCACG
                                                                                                                                                                                                                                                                                                                                                ATCCTGGATTACATCAATCTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAG
                                                                        AGCCTCTCCGTGCACTATAAGAAGGAACTCATCTCAACGGCATTCTCCAATGGAGGGTTT
                                                                                                                                                                                                       CTGGGAATCGGCATCACGGCTCTTTTTTTTCCTCTGCCTGATCATCATCATGAAGATT
                                                                                                                                                                                                                                                                                                                       ATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCTGGCTCAGAAGCGGAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAAGAACCAGAAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGGGGATTATGCAGAA
                                                    1186 AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTT
                                                                                                                                                                                     CTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGGCCCTGATCATCATCATGAGATT
                                                                                                                                                                                                                                                    CTACCGAAGAGAGGGACTCAGACAGAAACCCCGAGGCCCCAGGTTCTCCCGGCACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                       CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; transmembrane protein; PRO; EST; cytostatic; expressed sequence tag; detection; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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Score 1078.8; DB 2;
Pred. No. 9.3e-291;
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PR 30-DEC-1999; 99W0-US028551.
PR 30-DEC-1999; 99W0-US031095.
PR 30-DEC-1999; 99W0-US031243.
PR 30-DEC-1999; 99W0-US031243.
PR 505-JAN-2000; 2000W0-US030219.
PR 506-JAN-2000; 2000W0-US000219.
PR 506-JAN-2000; 2000W0-US000219.
PR 506-JAN-2000; 2000W0-US000217.
PR 506-JAN-2000; 2000W0-US000376.
PA 506-JAN-2000; 2000W0-US000376.
99US-0162506P.
99WO-US028313.
99WO-US028551.
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi GJ, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WI;

WPI; 2000-611443/58. P-PSDB; AAB44280 "Novel PRO polypeptides and polynucleotides used in detection methods, the arget bloactive molecules to specific cells, and to modulate cellular activities.

Claim 2; Fig 92; 636pp; English

AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the tract cells, e.g. for the treatment of cancers. The polypeptide provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78697 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences

Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;

120 240 105 165 180 225 285 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGCGATCCCGCCAAGGGGAAC 300 345 TGCTCCTTGGTGATCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360 405 420 9 286 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC TTCTGGATACGAGTGCAGGAGTCAGTGATGCCGGAGGCCTGTGCATCTCTGTGCCC 106 TTCTGGATACGAGTGAGGGGTCAGTGATGGTGCCGGAGGCCTGTGCATCTGTGTCCCC 166 recrerreceracececeachagaeregachegereraceceagerraregerrange TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 226 TICAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA TGCTCTTTCTCCTACCCCCGACAGGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 96; Gaps 70.2%; Score 1078.8; DB 3; Length 2764; 81.4%; Pred. No. 9.3e-291; iive 0; Mismatches 207; Indels 96; Owery Match Best Local Similarity 81.4 Matches 1329, Conservative 301 121 241 Н 46 61 181 406

421	GCCCTGACTCAGAAGCCTGATCTCTACATCCCCGAGACC	459 525
460	TOTAL	- 45 - 58 - 58 - 58
526	TTCTCCAGAAAGGGTGTGAGGCGCACAGAGGCCGTCCGTC	583
486	CATCTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCTTCTTTCT	12 70 12 12 12 12
546 646	GGCTGCCCTCTCCCAAGGAACCAAACCAACTCCCACTTCTCAGTGCTCAGCTT 	605 705
606	CACGCCCAGACCCCCAGGACCAC	641
642	CIGCCATGIGGACTICICCAGAAAGGGIGIGAGGGCACAGAGGACCGTCCGACTCCGIGT	701 825
702	GOCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCC	752 885
753	AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGGAACAGGACAGTC TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGGAAACAGGACAGTC	804 945
805	CTGGAAAACCTTGGGAACGCACGTCTCCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG	864 10.05
1006	GTCTGTGTCACACACAGCCCCCCCAGCCGGGCTGAGCTGGACCCGAGAGGGGACAGGTT	924
925	CTGAGCCCTCCCAGCCCTAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCTGCTCAGGTTCAAGTGGAGCTGCTCCGGGTTCTGGAGCTGCCTCGGGGTTCAAGTGGAGCTGCCTCCGGGTTCAAGTGGAG	984
985	CACGAAGGAGATTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC	1044
1045	AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT	1104
1105	CTGGGAATCGGCATCACGGCTCTTTTCCTCTGCCTCGCCCTGATCATCATGAAGATT 	1164
1165	CTACCGAAGAGAGACGGACTCAGAAACCCCGAGGTCTCTCCCGGCACAGGGTTCTCCCGGCACAGGACGGAGACGGAGACCGAAGAAACCCCGAGAGGCCCAGGTTCTCCCGGCACACAGACACGCAAGACCCAAGACACAAGACACAAGACAAGACAAGACAAAAACCCAAGACAAAAAA	1224 1365
1225	ATCCTGGATTACATCAATGTGCCCACGGCTGGCCCCCTGGCTCGGAAGCGGAATCAG	1425
1285	AAAGCAAAACATTCCTCGGACCCTCTTCCACAAGTGCTCCCTCC	1344
1345	345 AAGAAGAACAAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACT     40	1404

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                                                                                                                                   GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA 1665
CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polypeptide, mammal, tumour, cancer, human, cattle, horse, sheep, ss, dog, cat, pls, goat, rabbit, tumour necrosis factor alpha; TNF-alpha; blood, chondrocyte cell, cell proliferation, cell differentiation; colon; adrenal; lung, breast; prostate, rectum, cervix; liver, genetic disorder;
                                                    CAAGCCCCAGAATCCCAGGAGGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA encoding PRO polypeptide sequence #59.
                                                                                                                                                                                                                                                                                                                                                                                              AAS45983 standard; cDNA; 2764 BP
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2000US-0189320P.
2000US-0189328P.
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2000US-00644848.
2000WO-US023328.
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06-MAR-2000;
14-MAR-2000;
14-MAR-2000;
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primers for PRO polypeptides of the invention. The sequences of the primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal: Mammals include dogs, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contected with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotie probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                   and to
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                                                                                                                                                                                    Godowski PJ, Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTCTTTCTCCTACCCCCGACAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG
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                                                                                                                                                                                                                                                                                                                                      presence of tumors, such as prostate and breast tumors, in mammals screen for modulators of the compounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
70.2%; Score 1078.8; DB 4; Length
Best Local Similarity 81.4%; Pred. No. 9.3e-291;
Matches 1329; Conservative 0; Mismatches 207; Indels
                                                                                                                                                                                 L, Goddard A, Go
, Wood WI, Zhang
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Watanabe CK,
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.
                                                                                                                          INC.
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P-PSDB; AAU29082.
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                                                                                                                       (GETH ) GENENTECH
                                                                                                                                                                                    Baker KP,
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420 465

GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACC------

	RESULT 6 ACA63677 ID ACA63677 standard; cDNA; 2764 BP. XX AC ACA63677; XX		US2002192706-A 19-DEC-2002. 24-OCT-2001; 2 17-OCT-1997; 13-NOV-1997; 21-NOV-1997;	10 MAR 1998; 11 MAR 1998; 11 MAR 1998; 12 MAR 1998; 13 MAR 1998; 17 MAR 1998; 20 MAR 1998; 20 MAR 1998; 20 MAR 1998; 25 MAR 1998; 26 MAR 1998; 26 MAR 1998; 27 MAR 1998; 28 MAR 1998; 26 MAR 1998;	PR 27-MAR-1996; 98US-0075642. PR 27-MAR-1998; 98US-0075689P. PR 27-MAR-1998; 98US-007728P. PR 27-MAR-1998; 98US-007928P. PR 30-MAR-1998; 98US-007922P. PR 31-MAR-1998; 98US-007923P. PR 31-MAR-1998; 98US-0080165P. PR 31-MAR-1998; 98US-0080165P. PR 31-MAR-1998; 98US-0080194P. PR 01-APR-1998; 98US-0080134P. PR 01-APR-1998; 98US-0080334P. PR 08-APR-1998; 98US-0080107P.	08-APK-1998; 09-APK-1998; 09-APK-1998; 15-APK-1998;
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06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US005819.
      98US-0081838P-
98US-0081952P-
98US-0081955P-
98US-0082568P-
98US-0082569P-
98US-0082700P-
98US-0082700P-
98US-0082704P-
98US-0082704P-
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22-MAR-2001; 2001WO-US009552.
25-MAY-2001; 2001WO-US017092.
                                                                     98US-0082796P
                                                                                                         99WO-US005190
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09-JUL-2001; 2001WO-US021735
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17-MAY-2000; 2
22-MAY-2000; 2
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15. APR-1998,
21. APR-1998,
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66. JAN-1999,
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02-JUN-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
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## (GETH ) GENENTECH INC

DĽ; Shelton , Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen ME; Grimaldin TC, Gurney AL, Hillan KJ; Tapier NA, Pan J, Paoni NF, Roy MA, Shelt Williams PM, Wood WI; Napier MA, P. Williams PM, Ashkenazi AJ, Baker KP, B Ferrara N, Filvaroff E, F Goddard A, Godowski PJ, G Kljavin IJ, Kuo SS, Napie Stewart TA, Tumas D, Will

# WPI; 2003-328860/31, P-PSDB; ABU72232.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or

### 2; Fig 92; 453pp; English. Claim

The invention describes an isolated nucleic acid (I) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence off, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and

120 180 240 105 165 225 360 polypeptides are useful for treating inflammatory diseases, organ failure, atheroscherosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGGCCAAAGGGGAAC 345 405 420 465 885 9 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGGATCCCGCCAAGGGGAAC TTCTGGATACGAGTGCAGTGATGGTGCCGGAGGGCCTGTGTGCATCTGTGCCC rrcresaraceaerecaercaerearesresceseaecererecererererece recretriciceracececeachagaeregaeachgeachgeacheraceceaecharageeracreg TTCAAAGCAGTGACTGAGACAAGCGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 586 AGAGACCTIGITATCAGCATTTCACGTGACAACAGGCCAGCCCTGGAGCCCCAGCCCCAG GACAGCCACCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC CTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTGT 526 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCC GGCTGCCCTCCTCCCAAGGAACCAACCAACGACCTCCCACTTCTCAGTGCTCAGCTT GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT carcicridadactocriadactocriadaderioaceceadactoradaderioa descentracacerescendences de contra d GGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCC-----Gaps Length 2764; 96; TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTT 0 Other; GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACC------Score 1078.8; DB 8; Length Pred. No. 9.3e-291; 0; Mismatches 207; Indels Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; CACGCCCAGACCCCAGGACCAC------., Best Local Similarity 81.4%; Matches 1329; Conservative 70.2%; 166 46 61 106 121 181 226 241 301 346 460 286 361 406 421 466 486 646 909 902 642 994 702 753 ò g  $\dot{\delta}$  $\stackrel{>}{\circ}$ 셤 ò d ò 셤 엄 ద g Db 임 8 ò ò ò ò ò a ò ద

805 946 865 1006 925 1066 985 1126 1045 1186 1105 1,246 1165 1306

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9705-0063544P

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9705-0063744P

9705-0063744P

9705-006371P

9705-006371P

9705-006470P

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                           US2003036141-A1
Homo sapiens
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31-MAR-1998;
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TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRO polypeptide, secreted protein, transmembrane protein, chromosome mapping, gene mapping, tumour, adrenal, lung, colon; breast, prostate, rectal, cervical, liver, cancer, TMF-alpha, tumour necrosis factor-alpha, proliferation, differentiation, chondrocyte cell, bone disorder, cartilage disorder, sports injury, arthritis, cytostatic, antiarthritic, osteopathic, gene therapy, gene,
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                                                                                                                                                                                                                      CACGAAGGAGGTTCACCTGCCACGCTCGGCACCCATGGGCTCCCAGCACGTCTCTC
                                                                                                                                                                                                                                                            AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT
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                                                        creeaaaaccrresgaacescacercrececaeracresaesescaaaeccrerece
                                                                                                               ercrerencacacacaecececeasecasecrasecrasecrasaeceasecasecasecasecas
                                                                                                                                           CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG
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                             CTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG
                                                                                  GTCTGTGTCACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT
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GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTGTAAAAGTAACA 420 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGCAGGGCCTGTGCATCTGTGCCCCCCTTTTTCTGGATACGAGGCCTGTGCATCTCTGTGCCCCGAGGGCCTGTGCATCTCTGTGCCCC GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG TGCTCCTTGGTGATCAGAGACGCGCAGATGAGCAGGATGAGTCACAGTACTTCTTCGGGTG Gaps 96; Length 2764; Query Match
70.2%; Score 1078.8; DB 8; Length
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GTGCTCAGCTTCACGCCCAAACCCACAAACAACAACAACAAACA
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CATCTGTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTTCT
GGCTGCCCTCTCCCCAAGGAACCAAACAAAGACCTCCCACTTCTCAGTGCTCAGCTT 605
CACGCCCAGACCCCAGGACCAC
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CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGGGCTCCATTATGCCACGCTCAACTTCCA 1464 

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1465 GGCGTCAGACCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA 15 1606 GGCGTCAGACCTGAGGCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAGAA 16 1525 GTCAAGTTCCAA 1536 1666 GTCAAGTTCCAA 1677	T 8 ACA73443; ACA73443; 01-JUL-2003 (first entry) Human secreted/transmembrane protein (PRO) cDNA #59. Human, ss; gene; secreted protein; transmembrane protein; PRO; tumour; proliferation; differentiation; chondrocyte cells; tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.  US20033036146-Al.	26-JUN-1998; 98US-00105413.  16-SEP-1998; 98US-00105413.  07-OCT-1998; 98US-00105318.  07-OCT-1998; 98US-00105318.  07-OCT-1998; 98US-00105318.  06-NOV-1998; 98US-0010336.  01-DEC-1998; 98US-0010336.  08-MAR-1999; 98US-002052114.  08-MAR-1999; 98US-00205231.  14-MAY-1999; 98US-002053113.  15-MUS-1999; 99US-0030134.  25-MUS-1999; 99US-0030134.  25-MUS-1999; 99US-0030138.  25-MUS-1999; 99US-0030138.  25-MUS-1999; 99US-0030139.  25-MUS-2000; 2000WO-US016414.  27-ERB-2000; 2000WO-US016414.  27-ERB-2000; 2000WO-US016414.  27-MAR-2000; 2000WO-US01378.  18-ESB-2000; 2000WO-US01378.
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Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;

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01-DEC-2000) 2000WO-US030552.
20-DEC-2000) 2000WO-US032678.
22-MAR-2001) 2001WO-US034956.
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10-MAY-2001) 2001US-00854208.
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30-JUL-2001) 2001WS-009294419.
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P-PSDB; ABU86251.
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(GETH ) GENENTECH INC

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.

Claim 2; Fig 117; 707pp; English

The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide corrected and transformed with hor lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO proteins, PRO system of the proteins of this action comprising the vector (used to produce PRO proteins), a chimaeric molecule comprising the PRO proteins), a chimaeric molecule comprising the PRO proteins of the protein of proteins of the proteins of the proteins of the proteins of the protein of the prote

Query Best ] Match	Match Local Similarity 81.4%; Pred. No. 9.3e-291; ies 1329; Conservative 0; Mismatches 207; Indels 96; Gaps 3;
ò	TACTGCCACTGCTGCTGCTCGCTGCTGCTGGGCGGGTCCCAGGCTATGGATGG
q	
70	61 ITCTGGATACGAGTGAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120
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ò	121 IGCICTITICICCTACCCCGGACAGGACAGGGICTACCCCAGCTIAIGGCTACTGG 180
QQ	CTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTG
ò	181 TTCAAAGCAGTGACTGAGACCAAGCGTGCTCTGTGGCCACAAACCACCAGAGTCGA 240
qq	CAAAGCAGTGACTGAGACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCG
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ДQ	3TGGAAATGAGCACCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCCAAGGGGAA
δ	301 IGCTCCTTGGTGATCAGAGACGCGCAGATGAGTCACAGTACAGTACTTCTTTCGGGTG 360
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ò	421 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACC
qq	TGCTCAGCTTCACGCCCAGACCCCAGACAACA
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qq	GTCCGACTCCGTGTGGO
δλ	486 CAICTGIGIGITIAACTGGGCCTTIGAGGAAIGTCCACCCCCTTCTTTTCTCTGGACGGG 545
qq	rharcagcarrrcacgrdacaacacgccagccrggagccd
ζζ	CTCCTCCCAAGGAACCAAACCAACGACTCCCACTTCTCAGTGCTCAGCT
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ò	606 CACGCCCAGACCCCAGGACCAC
QQ	CAGCCACCCCTGCCACA
ζ	CATGIGGACTICIC
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qq	scartacaccacacacaaaacaadcartaactcccagcaacaacaa
λŏ	CCAGAGAACCT
ΩÞ	CTCCAGAGAACCTGAGATGATTCCCCAAGCAAACAGGACAGT
δ	805 CTGGAAAACCTTGGGAACGGCACGTCTCCCAGTACTGGAGGCCCAAAGCCTGTGCGG 864
QQ	ddaaaactiidddaacddcaccictciccadiaciiddadddcaaaadcciididc
ò	865 GTCTGTGTCACACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 924
QQ	ctereficacacacacacacacacadaaaaaaaaaaaaaaaaaaa

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New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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2001US-00874503.
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99US-00380137.
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2001US-00866028.
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2001US-00918585,
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25-MAY-2001;
01-JUN-2001;
05-JUN-2001;
20-JUN-2001;
29-JUN-2001;
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05-JAN-2000;

18-FEB-2000;

18-FEB-2000;

24-FEB-2000;

24-FEB-2000;

01-MAR-2000;

01-MAR-2000;

15-MAR-2000;

15-MAR-2000;

15-MAY-2000;

22-MAY-2000;

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15-JAN-2002;
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                                                                                                                                                                                                                         AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT
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06-NOV-1998;
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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the FRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TWF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for stimulating the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligomuclootide probe derived from any of the PRO molecules sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the proliferation or differentiation of chondrocytes and detecting the proliferation or differentiation of chondrocytes and detecting the proliferation or differentiation of chondrocytes and collidating the proliferation or differentiation of chondrocytes and collidating may also be used diagnostically for tissue typing. The sequences presented in ACAOSTOO-ACAOSCOO4 are the cDNAs encoding the PRO polypeptides of the invention Fig  $\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\cup}\overset{\circ}{\smile}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}$ 

Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;

TGCTCTTTCTCCTACCCCCGACAGGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180 240 420 545 605 300 345 459 485 585 645 165 285 recreeringerearcasacsessarscassarscassarscassarscreerings 405 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGCCTGTGCATCTCTGTGCCC TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCACAGAGTGGA GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGAAC TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA TGCTCCTTGGTGATCAGAGGCGCGGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 526 TICICCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCC CATCTGTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTCTCTCGACGGG TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGCCCTGTGCATCTCTGTGCCC GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC dracirchactroaddccanacccchagadcachahchchagaccrongcargagac -----CTGGAGCCCGGGCAGCCGGTGACGGT GGCTGCCCTCTCCTCCCAAGGAACCAAACCAACGACCTCCCACTTCTCAGTGCTCAGCTT gaaatgroccataccrgaaagcccaaaaagcccagtrocrgcgccrgccr Gaps Length 2764; 96; Query Match
70.2%; Score 1078.8; DB 8; Length
Best Local Similarity 81.4%; Pred. No. 9.3e-291;
Matches 1329; Conservative 0; Mismatches 207; Indels GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACC 46 61 121 166 226 241 286 301 346 361 406 460 546 646 106 181 121 qq 8 8 8 8 & 8

1245 1164 1224 1365 1344 1485 1404 1545 1464 1005 1044 1104 1284 1065 765 701 752 945 864 CTGAGCCCCTCCCAGCCCTAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 946 CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGTGCTG CTACCGAAGAGACGCACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACG CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1606 GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCCAGGCGGATTATGCAGAA 706 GACAGCCCAGCCCCCTGCCACACTGAGTCCTGCAGAACAGAGTCCTCTCCTCGTCC CTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGGTGAAGGCTGGGGATTCA gecceracacecaacegaacaacaacracecreccaacaacaaccec CTGGAAAACCTTGGGAACGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG GTCTGTGTCACACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT GTCTGTGTCACACACACAGAGCCCCCCAGCCAGGCTGAGCTGGAGCCCAGAGGGGACAGGTT AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAATGGAGCGTTT 1186 AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCAACGGAGCGTTT CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCCAGGTTCTCCCCGGCACAGACAC AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAAATCATCCACT CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA GGCGTCAGACCCAGGCCTGAGGCCCCGGATGCCCAAGGGCACCCAGGCGATTATGCAGAA GGCCTATGCCCCCCAGAGCCTTGTTATCAGCATTTCACGTGACAACACGCC CACGCCCAGACCCCAGGACCAC GTCAAGTTCCAA 1677 1366 994 1006 9901 1126 1045 1105 1246 1165 1306 1225 1285 1426 1345 1486 1405 1546 1525 1465 642 702 826 865 925 985 909 g ∂ Op ò 음 8 ద  $\delta$ d 8 g  $\delta$ 엄 8 & 장염 ò q 8 셤 8 셤 8 g 8 8 8 엄 참 원 S 8

ACA66592 standard; cDNA; 2764 RESULT 10
ACA66592
ID ACA6

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The invention relates to three hundred and five nucleic acids encoding. Pro Dolypeptides (Secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or trearment of tumours, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The RNO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of thuman cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a cDNA encoding a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                      Three hundred and five nucleic acids encoding secreted and transmembrape
                                                                                                                                                                                                                                                                                                    PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumors.
                                                                                                                                                                                        Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Length 2764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;
                                                                                                                                                                                        Goddard A, Godowski PJ,
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1078.8; DB 8; Length
Pred. No. 9.3e-291;
0; Mismatches 207; Indels
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                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 117; 708pp; English.
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          30-JUL-2001, 2001US-00918585.

06-AUG-2001, 2001US-00924419.

13-AUG-2001, 2001US-00929404.

16-AUG-2001, 2001US-00931836.

28-AUG-2001, 2001WG-00941992.

29-AUG-2001, 2001WG-05941997.

04-SEP-2001, 2001WG-05941997.
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ilarity 81.4%;
Conservative 0
2001US-00908B27
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                                                                                                                                                                                          Chen J,
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Matches 1329;
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                                                             gagona encoding human PRO protein #59.
                                                                                              Human, tumour, adrenal, lung, color
liver, PRO, gene therapy, gene, ss
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98WO-US019330.
98US-00168978.
98WO-US021141.
98US-00187368.
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99US-00423844.
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2001WO-US021735
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                                   entry)
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22-MAY-2000;
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300

345 360 405 420

240 285

180

1665

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KW Human, PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha, TWR-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antlarthritic; vulnerary; gene therapy; gene; ss.
                           GGGGTCAGACCCAGGCCTGAGGCCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA
               GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA
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Pred. No. 9.3e-291;
0; Mismatches 207;
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98US-0101472P.

98US-0101473P.

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98US-0102240P.

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98US-0102311P.

98US-0102311P.

98US-0102570P.
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Best Local Similarity 81.4%;
Matches 1329; Conservative
18 - SEP - 19998,

18 - SEP - 19998,

23 - SEP - 1998,

23 - SEP - 1998,

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28 - MAY - 1598 | 28 - MAY - 1598 | 28 - MAY - 1598 | 28 - MAY - 1598 | 20 - UUN - 1
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   Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha; chimour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; etissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                    Human secreted/transmembrane protein (PRO) cDNA #59.
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9705-0059266P.
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29-APR-1998;
05-MAY-1998;
06-MAY-1998;
07-MAY-1998;
                                                                                                                                              Homo sapiens
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29-APR-1998;
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22-APR-1
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301 TGCTCCTTGGTGATCAGAGACGCGCAGATGAGTCACGTACTTCTTTCGGTG 360 346 TGCTCTTGGTGATCAGAGACGCGCAGATGAGATGAGTCACTACTTCTTCGGTG 360 346 TGCTCTTGGTGATCAGAGACGCGCAGATGAGATGAGATACTACTTTCTTGGTG 405 361 GAGAGAGAGCTATGTGAGATATACTTTCATGAAGATACTACA 420 406 GAGAGAGGAAGCTATGTGAATATTTCATGAACGATGGTTCTTTCT	586 AGAGACCTIGTTATCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCAGCCCCACCCAGCCCCACCCAGCCCCACCCAGCCCCCACCCAGCCCCCC	925 CTGAGCCCTCCAGACCCCGGGGTCTGGAGCTCCGGGGTTCAAGTGGAG 1066 CTGAGCCCTCCCAGCCCTCGAGCCCTGGAGCTCCTGGGGTTCAAGTGGAG 1126 CTGAGCCCTCCCAGCCCTGGCAGCCTCGGAGCTCCTCGGGTTCAAGTGGAG 1127 CACGAAGGAGATTCACCTGCCAGCTCGCACTGGGCTCCCAGCACGTCTCTCT 104 CTGGAAGGAGTTCACCTGCCAGCTCCACTGGGCTCCCAGCACGTCTCTCT 1104 CACGAAGGAGTTCACCTGCAGCTCATCTCAAGGGCTTCTCTCT 1105 CACGAAGGAGTTCACCTGCAGCTCATCTCAAGGGCTTT 1106 CTGGGAATCGGCACTATAAGAAGGAACTCATCTCCAACGGCATTT 1107 CTGGGAATCGGCATCACGGCTTTTTCCTCTGCCTGGCCTTTTCCCAACGGAGCTTT 1108 CTGGGAATCGGCATCACGGCTTTTTTCCTCTGCCTGGCCTTGATCATCAAGAGATT 1109 CTGGGAATCGGCATCAGGCTCTTTTTTCTCTCTGCCTGGCCTGATCATCATGAAGATT 1106 CTGGGAATCGGCATCAGACAGAAACCCCGAGGCCCTGATCATCATGAAGATT 1107 CTGGGAATCGGCATCAGACAGAAACCCCGAGGCCTGATCATCATGAAGATT 1108 CTGCGGAATCGGCATCAGACAGAAACCCCGAGGCCTGATCATCATCAAGACAGCAGAATT 1108 CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCTGGTTCTCCCGGCACAGCACG 1110 CTACCGAAGAGACCGACTCAGACAGAAACCCCGAGGTTCTCCCCGGCACAGCACG 1110 CTACCGAAGAGACCGACCCGAGGCCCCCAGGCTCCCCGACACACAC
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		Length 2764;   Indels 96;   Gaps 3;   Indels 96;   Gaps 3;   TCCCAGGCTATGGATGGAGA 105   GGCTGTCCATGTTCTGTGCC 120   GGCTGTGCATCTGTGCC 120   GGCTGTGCATCTGTGCC 165   GGCTGTGCATCTGTGCC 165   GGCTGTGTGCTATGGCTACTGG 180   GGCACAAACCACAGAGTCGA 240   GGGGATCCCCCAGAGTCGA 240   GGGGATCCCCCAAGAGTCGA 245   GGGGATCCCCCCAAGAGTCGA 245   GGGGATCCCCCCAAGAGTCGA 245   GGGGATCCCCCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGGAAC 345   GGGGATCCCGCCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGGAAC 345   GGGGATCCCGCCAAGAGGAGAC 345   GGGGATCCCGCCAAGAGGAGAC 345   GGGGATCCCGCCAAGAGGAGACCAAAC 345   GGGGATCCCGCCAAACGGGAAC 345   GGGGATCCCCGCCAAACGGGAACC 345   GGGGATCCCCGCCAAACGGGAAC 345   GGGGATCCCCCCAAACGGGAAC 345   GGGGATCCCCCCCAAACGGGAAC 345   GGGGATCCCCCCAAACGGGAAC 345   GGGGATCCCCCCCAAACGGGAAC 345   GGGGATCCCCCCCAAACGGGAAC 345   GGGGATCCCCCCCAAACGGGAAC 345   GGGGATCCCCCCCAAACGGGAACCCAAACGGAACCCAAACGGAACCCAAACGGGAACCCAAACGGAACCCAAACGGAACCCAAACGGAACCCAAACGGAACCCAAACGGAACCCAAACGAACCCAAACGAACCCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACCAAACAACAAACCAAAA
<u>வ</u> ் தி கி கி கி கி கி கி		Score 1078.8; DB 8; Les Pred. No. 9.38-291; 0; Mismatches 207; Ind CTGTCCTGGTGGGGGGGGTCCCA CTGTCTGGTGGGGGGGGGG
98US-0097952P. 98US-0097954P. 98US-0097955P. 98US-0097971P. 98US-0098014P. 98US-0098014P. 98US-0098014P. 98US-0098018P. 98US-009872P. 98US-009872P. 98US-0099741P. 98US-0099741P. 98US-0099741P. 98US-0099784P. 98US-0099784P. 98US-0099784P. 98US-0099784P.	98US-0100664F. 98US-0100664F. 98US-0100664F. 98US-0100664F. 98US-01006930P. 98US-0100849P. 98US-010168P. 98US-0101477P. 98US-0101477P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-0101738P. 98US-010227P. 98US-010224P. 98US-0102240P. 98US-0102240P. 98US-0102240P. 98US-0102570P. 98US-0102571P.	10.2%;   Score 1078.8;   DB 8;   Inservative   0;   Mismatches   207;   Inservative   207;   Mismatches   207;
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	16-SEP-1998 9 98US-01100644F. 16-SEP-1998 9 98US-01100644F. 17-SEP-1998 9 98US-01100643F. 17-SEP-1998 9 98US-01100649F. 17-SEP-1998 9 98US-01100649F. 18-SEP-1998 9 98US-01101044F. 18-SEP-1998 9 98US-01101044F. 23-SEP-1998 9 98US-01101047F. 23-SEP-1998 9 98US-01101475F. 23-SEP-1998 9 98US-01101475F. 24-SEP-1998 9 98US-01101738F. 24-SEP-1998 9 98US-01101738F. 25-SEP-1998 9 98US-0101738F. 25-SEP-1998 9 98US-0101738F. 25-SEP-1998 9 98US-0101738F. 25-SEP-1998 9 98US-0101738F. 26-SEP-1998 9 98US-0101738F. 26-SEP-1998 9 98US-0101738F. 26-SEP-1998 9 98US-0102240F. 29-SEP-1998 9 98US-010234F. 29-SEP-1998 9 98US-010257F. 20-CT-1998 9 98US-0102564F.	10.2%;   Score 1078.8;   DB 8;   DB 8;   Conservative   0;   Mismatches   207;   1   ATGCTACTGCTGCTGCTGCTGGGGGGGTCCTGCTACTGCTGCTGCTGGGGGGGG

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9805-0080127P.
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9805-0083496P.
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 Additional, PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
Chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnerary; gene therapy; gene; ss.
            1345 AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAAATCATCCACT
                                                                1486 AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACT
                                                                                      CAAGCCCCAGAATCCCAGGAGAGCCAAGAAGGAGCTCCATTATGCCACGCTCAACTTCCCA
                                                                                                                                                                                                                                                                                                                     Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117
                                                                                                                                                                                                                                                       ACF13006 standard; cDNA; 2764 BP
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Sag	<pre>uery Match 70.2%; Score 1078.8; DB 8; Length 2764; est Local Similarity 81.4%; Pred. No. 9.3e-291; atches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps</pre>	m
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79	TCAGAGACGCGCAGATGCAGGATGAGT	360
СD	CTCCTTGGTGATCAGAGGCGCGCAGATGCAGGATGAGTCACAGAGATCTTTTCGG	405
à	SCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCTAA	420
d D	CTATGTGACATATAATTTCATGAACGATGGGTTCTTT	465
à	421 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACC	459
DD DD	cagaccccaggaccacaacac	525
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à	486 CAICTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCTTCTTTCT	545
e e	586 AGAGACCTIGITATCAGCATTTCACGTGACACACGCCAGCCCTGGAGCCCCAGCCCCAG	645
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              GTCTGTGTCACACACACAGCCCCCAGCCAGGCTGAGCTGGACCCAAAGGGGGAACAGGTT
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                                           GTCTGTGTCACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGACAGGTT
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Homo sapiens

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US-09-038-83-3

Sequence 3, Application US/09038832

Sequence 3, Application US/09038832

RENEAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: BICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-2

TITLE OF INVENTION: Sialoadhesin Family Member-2

TITLE OF INVENTION: Sialoadhesin Family Member-2

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: PASSES:

ADDRESSER: PASSES:

ADDRESSER: PASSES:

COUNTRY: USA

ZIP: 1948

COMPUTER: PAS DESKETE

COMPUTER: PASSES:

ATORITY: APPLICATION DATA:

APPLICATION NUMBER: US/09/038,832

FILING DATE: 11-MAR-1998

CLASSIFICATION NUMBER: 60/041,886

FILING DATE: 10-APR-1997

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: GH-50018

TELEFAX: 610-407-0701

TELEFAX: 610-407-0701

TELEFAX: 610-407-0701

TELEFAX: 610-407-0701

TELEFAX: 11-31

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US-08-541-780-11
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1 US-09-115-446-5
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1 US-09-115-446-5
1 US-09-115-446-5
1 US-09-116-448-5
1 US-09-114-085-3
1 US-09-144-085-3
1 US-09-144-085-3
1 US-09-144-187
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Matches 666; Conservative
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                                                              APPLICANT: KIKLY, KRISTINE
APPLICANT: KIKLY, KRISTINE
APPLICANT: BRICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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23.8%; Score 364.8; DB 3;
Best Local Similarity 62.1%; Pred. No. 4.1e-96;
Matches 666; Conservative 0; Mismatches 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/09/038,832
11-MAR-1998
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FILING DATE: 02-APR-1997
ATTORNEY AGENT INFORMATION:
NAME: PRESTIA, PAUL F
3.09-038-832-1
Sequence 1, Application US/09038832
Patent No. 6146845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 11-MAR-199
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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; MOLECULE TYPE: CDNA
US-09-038-832-1
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Pred. No. 8.4e-87;
0; Mismatches 366;
FILING DATE: 21-15.

CLASSIFICATION 514

PRIOR APPLICATION NUMBER: 60/041,885

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTING PAUL F

REGISTRATION NUMBER: 23,031

REFIRENCE/DOCKET NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-5001

TELEFAN: 610-407-0701

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Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
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COUNTY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TGCTCTTTCTCCTACCCCGACAGGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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21.2%; Score 325.2; DB 4;
Best Local Similarity 59.3%; Pred. No. 1.2e-84;
Matches 629; Conservative 0; Mismatches 368;
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APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REPERENCE: 1488.0480001
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR PILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
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Seguence 1, Application US/08896537A
Patent No. 6590088
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NAMPKEY: COS.
LOCATION: (37). (1689)
CTHER INFORMATION:
NAMPKEY: sig.petide
LOCATION: (37). (81)
CTHER INFORMATION:
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LENGTH: 2027
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (82)..()
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OTHER INFORMATION:
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552 ACCTGACCTGCTCTGTGCCCTGGGTCTGTGAGCAGGGAACACCCCCCATCTTCTCCTGGA 611
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APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: 1508
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 602 GCTTCACGCCCAGACCCCAGGACCACACACGACCTCACCTGCCATGTGGACTTCTCCA
                                                                                                                                          542 CGGGGGCTGCCCTCCTCCCAAGGAACCAAACCAACGTCCCACTTCTCAGTGCTCA
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Pred. No. 8e-72;
0; Mismatches 290; Indels
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24304
COMPT : 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
CO
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Patent No. 6607879
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-O
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 1.4e-73;
0; Mismatches 230; Indels 10;
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ITLE OF INVENTION: No. 6569662el Nucleic Acids and
ITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: US/09/620,312D
FRIOR APPLICATION NUMBER: 09/522,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER: OF SEQ ID NOS: 1105
SEQ ID NO 407
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Best Local Similarity 66.0%;
Matches 465; Conservative
                                                          Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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John Tillinghast
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
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; LOCATION: (146)..(931)
US-09-620-312D-407
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RESULT 8
US-09-046-736-3
                                                                    NAME/KEY:
LOCATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                    TICTGGCTGCAAGTGCAGTGACGGTACAGGAGGGTTTGTGCGTCCTCGTGCCC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCAAAGCACTGACTGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA
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784 GTT 786
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                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 190.8; DB 4; Length 192; 98.4%; Pred. No. 6e-46;
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| Patent NO. 6090582 | GENERAL INFORMATION: APPLICANT: KIKLY, KRISTINE | APPLICANT: KIKLY, KRISTINE | TITLE OF INVENTION: Sialoadhesin Family Member - TORRESPONDENCE ADDRESS: ACRESPONDENCE ADDRESS: ADDRESSES: ACREST RAIDER & Prestia STREET: P.O. Box 980 | CITY: Valley Forge
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILLING DATE: 24-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          LOCATION: 28
CTHER INFORMATION: Xaa=His or Gln
US-09-513-999C-3082
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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REGISTRATION NUMBER: 2
                                                            LOCATION: 12
OTHER INFORMATION: 8=g
                                                                                                                                                                                                                            LOCATION: 105
OTHER INFORMATION: s=g
                                                                                                                                                                 OTHER INFORMATION: s=g
                                           NAME/KEY: misc_feature
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Oloclert, J.Y.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.pm SEQ ID NO 3082 LENGTH: 192

TYPE: DNA ORGANISM: Homo sapiens

Requence 3082, Application US/09513999C Patent No. 6783961

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NAME/KEY:
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US-09-513-999C-522

US-09-513-999C-522

Sequence 522, Application US/09513999C

Patent No. 678361

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

TILE APPLICANT: Glordano, J.Y.

TILE REPRENCE: 59-US2. MS.

PATENT SPILOATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 522

LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                               Length 1502;
                                                                                                                                                                                                                                                                                                            10.1%; Score 154.8; DB 3; Length 1 63.8%; Pred. No. 5.2e-35; tive 0; Mismatches 142; Indels
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    GH-50019
REFERENCE/DOCKET NUMBER: GH
TELECOMMINICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
TELEX:
                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            Query Match 10.1
Best Local Similarity 63.8
Matches 272; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                            / STORY INDEAR / STORY INDEAR / MOLECULE TYPE: CDNA US-09-046-736-3
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62 ATGCTACTGCCACTGCTGCTGTCMTCGCTGCTGGCGGGTCCCAGGCTATGGATGGGAGA 121
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10.0%; Score 153.6; DB 4
Best Local Similarity 97.6%; Pred. No. 4.6e-35;
Matches 164; Conservative 2; Mismatches 1
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APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gesen, Craig A.
FILE REPERENCE: 1488.0480001
CURRENT APPLICATION WUMBER: US/08/896,537A
CURRENT APPLICATION WUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 11
SEQ ID NO 11
LENGTHER.
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OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc_feature
                                                                                                                                                  LOCATION: 62.7109
OTHER INFORMATION: SCORE 11.3
OTHER INFORMATION: SEQ PLLLSSLLGGSQA/MD
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Patent No. 6590088
GENERAL INFORMATION:
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NAME/KEY: UNSURE

LOCATION: 24

OTHER INFORMATION: Xaa=Ala or Ser
US-09-513-999C-522
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LOCATION: (10)..(10)
OTHER INFORMATION: May be an
NAME/KEY: misc_feature
LOCATION: (26)..(26)
OTHER INFORMATION: May be an
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 85
OTHER INFORMATION: m=a or
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LOCATION: 179
OTHER INFORMATION: k=g or
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NAME/KEY: misc_feature
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                                                                                                                 sig_peptide
62..23
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US-08-896-537A-11
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410 TAMANGTAN CAGCCCTGACTCAGANGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCG 469
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                                                                                                                                                                                                                                      231 CCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGC 290
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                                                                                                                                                    171 TGGCTACTGGTTCAAAGCAGTGACTGACAACCAAGGGTGCTCCTGTGGCCACAAACCA
                                                                                                                                                                                                                                                                               64 eccadacadaadadadeccadadaccaddeccaniccdccifccridddangrea
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                                                           Length 459;
                                                               6.1%; Score 93.4; DB 4; Length 4
58.6%; Pred. No. 2.3e-17;
tive 0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: BSTS and Encoded Human Proteins. FILE REPRENCE: GENORT: 054PR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm.
; OTHER INFORMATION: May be any nucleotide US-08-896-537A-11
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Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, J.B
                                                                  Query Match
Best Local Similarity 58.6
Matches 177; Conservative
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512 AGGAATGTCCACCCCTTCTTTCTCTGGACGGGGCTGCCCTCTCCTCCTAGGAACCA 571

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Sequence 45, Application US/09286904A

GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Marde, William A.
APPLICANT: Moria, Pamela S.
APPLICANT: Nero, Pamela S.
APPLICANT: Nore, Pamela S.

                                                                                                                   572 AACCAACGACCTCCCACTTCTCAGTGCTCAGCTTCACGCCCAGACCCCAGGACCACGACA 631
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Length 3132;
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APPLICANT: Gaarde, Willam A.

APPLICANT: Moro, Forbert

APPLICANT: Noro, Forbert

TITLE OF INVENTION: Antisense Modulation of p38 Mitogen

TITLE OF INVENTION: Antisense Protein Kinase Expression

FILE REFERENCE: ISPH-0488

CURRENT APPLICATION NUMBER: US/09/640,101

CURRENT FILING DATE: 2000-08-15

PRIOR FILING DATE: 1999-04-06
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2.6%; Score 39.6; DB 3;
Best Local Similarity 53.2%; Pred. No. 0.29;
Matches 84; Conservative 0; Mismatches 74;
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U73142
; DATABASE ENTRY DATE: 1996-10-22
US-09-286-904-45
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Patent No. 6448079
                                                                                                                                                                                                                                                                                  532 CCGACCTCACCTGCCA 647
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APPLICANT: Monia, i
APPLICANT: Gaarde,
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NAME/KEY: CDS
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITION: AFRUGATNOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888 CCCAGCCAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGA 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 rejecrosadeseceradadesecrarerenenes accesados es refecesas es es es es estados es es es estados es es esta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CCGAGCCGTAGGCTCCCGAGCCCACCGGGACAGGTTCTGGTATCGCTCGGGCACCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838 GTACTGGAGGCCAAAGCCTGTGGTCTGTGTCACACACAGCGCCCCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                    Length 3132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 38; DB 4; Length 633;
45.2%; Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    948 CCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGC 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AGACGGTCTTGTTCAGCTCCTGCCGGTAGAACGTGGGC 26
                                                                                                                                                                                                                                                                                                                                                              Ouery Match
2.6%; Score 39.6; DB 4;
Best Local Similarity 53.2%; Pred. No. 0.29;
Matches 84; Conservative 0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-1373
; Sequence 1373, Application US/09252991A
; Patent No. 6551795
                                                                                                TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (12)..(1094)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U73142
DATABASE ENTRY DATE: 1996-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Pseudomonas aeruginosa
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
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                      SOFTWARE: Pate
SEQ ID NO 45
LENGTH: 3132
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Matches 140;
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Sequence 1196, Application US/09252991A
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Sequence 1196, Application US/09252991A
Sequence 1196, Application
Sequence 1196, Application
Sequence 1100
Sequence 110
1078 TCAACGCCATTCTCCAATGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTTCCTC 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 garccedecingecedardardarandederaradedecededededededededede 565
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                                                                                                           386 GTACCCCGGTGGCCCTGGAAGCGGTGATGTCCAACGACACCTGGGAGCTGGTCTACGAC 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: November 8, 2004, 20:38:22 Job time: 173.477 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1138 TGCCTGGCCC 1147
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APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Witney, Gena
TITLE CANT: Witney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REPERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
LENGTH: 2565
US-09-981-915A-258
US-09-978-824-258
US-09-999-834A-258
US-09-999-834A-258
US-09-999-830A-258
US-09-999-830A-258
US-09-999-830A-258
US-09-978-123A-258
US-09-978-123A-258
US-09-978-128A-258
US-09-978-65A-258
US-10-176-758-1177
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Pred. No. 0;
0; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                  US-10-174-581-117
US-10-176-483-117
                                                                                                                                                                                                                                                                                                                                                            US-10-176-749-117
US-10-176-914-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09910600 Publication No. US20030036631A1 GENERAL INFORMATION:
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  TYPE: DNA
ORGANISM: Homo sapiens
US-09-910-600-1
 Query Match
Best Local Simi
Matches 1331;
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US-09-910-600-1
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1: \cgn2_6/ptodata/1/pubpna/PCT_PUBCOMB.seq:*

2: \cgn2_6/ptodata/1/pubpna/PCT_MBW PUB.seq:*

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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-99-832A-258
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Listing first 45 summaries
                                                                nucleic search, using sw model
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1329 CTGGGAATCGGCATCATCTTTTCCTCTGCCTGGCCTGATCATCATCATCATCATCATCATCATCATCATCATCATCA	UG-09-798-258  UG-09-798-258, Application US/0997625A  Factor Co. US/200156006A1  FAPILICANT SARkerazi, Avi  APPLICANT Bakerazi, Avi  APPLICANT Bakerazi, Avi  APPLICANT Bakerazi, Avi  APPLICANT Bakerazi, Avi  APPLICANT Bacter, David  APPLICANT Gacue, Dan  APPLICANT Gerber, Hangelen  APPLICANT Gradudid, Christopher  APPLICANT Goddard, Augein L.  APPLICANT Goddard, Augein L.  APPLICANT Hillan, Kenneth J.  APPLICANT Hillan, Kenneth J.  APPLICANT Hillan, Kenneth J.  APPLICANT Sophia S.  APPLICANT Sophia P. Mickey  APPLICANT Sophia P. Mickey  APPLICANT Pani, Micholas F.  APPLICANT Soldid, Allien I.  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  TITLE OF INVENTION: Secreted and Transmembran Papplicant Millians, P. Mickey  APPLICANT Willians, P. Mickey  APPLICANT WHISTON: Secreted and Transmembran Papplicant FILMS DATE: 2001-10-15  PRIOR APPLICATION NUMBER: US/09/978-255A  PRIOR FILING DATE: 1201-10-15  PRIOR APPLICATION NUMBER: G0/064250  PRIOR APPLICATION NUMBER: G0/064220
	\$46 GGCTGCCCTCTCCCAAGGAACCAAACCAACCACCTCCCATTCTCAGTGCTCAGTGTCTCAGTGCTCAGTGCTCTCTCAGTGCTCTCTCT

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PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081919
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PRIOR APPLICATION NUMBER: 60/08256
PRIOR APPLICATION NUMBER: 60/08269
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PRIOR PELING DATE: 1998-04-22
PRIOR PELING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08200
PRIOR APPLICATION NUMBER: 60/08200
PRIOR PELING DATE: 1998-04-22
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PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-05-07
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Patent No. US20020169284A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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        PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
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A PELLING DATE: 1998-03-31

SR FILING DATE: 1998-03-31

SR APPLICATION NUMBER: 60/080127

SR APPLICATION NUMBER: 60/080327

SR APPLICATION NUMBER: 60/080333

SR FILING DATE: 1998-04-01

SR APPLICATION NUMBER: 60/080334

SR FILING DATE: 1998-04-01

SR APPLICATION NUMBER: 60/080334

SR FILING DATE: 1998-04-01

SR APPLICATION NUMBER: 60/081019

SR FILING DATE: 1998-04-08

SR FILING DATE: 1998-04-09

SR FILING DATE: 1998-04-15

SR FILING DATE: 1998-04-22

SR FILING DATE: 1998-0
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APPLICANT: Wood, Williams, P. Wickey
APPLICANT: Wood, William, P. Wickey
APPLICANTON : Wood, William, P. William, I.
CURRENT PELLOR DATE: 2001-01-09
PRIOR FILLING DATE: 2001-01-09
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1996-10-17
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, Audrey
Goddward, Audrey
Grimaldi, J. Christopher
Grimey, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kujavin, Ivar J.
Nupier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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us-09-937-636-1.rnpb	### CATCOLOGY NOTICES   1995 64-13   ### CATCOLO
Tue Nov 9 08:29:57 2004	INTERPRETATION APPLIES

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A PAPLICATION NUMBER: 60/078339

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/07839

R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-20

R FILING DATE: 1998-03-25

R FILING DATE: 1998-03-25

R FILING DATE: 1998-03-26

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APPLICATION NUMBER: 60/082700
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APPLICANT: Tuenedy A.
APPLICANT: Tuened Daniel
APPLICANT: Tuened Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acade Encoding the Same
FILE REFERENCE: P2630PDC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: (00/06250
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: (00/07764)
PRIOR PLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: (00/07764)
PRIOR PLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: (00/07764)
PRIOR PLING DATE: 1998-03-11
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                                                                                                                                                   CAAGCCCCAGAATCCCAGGAGAGCAGAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1464
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 258, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Beton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerriteen, Manspeter
APPLICANT: Gerriteen, Manspeter
APPLICANT: Geddard, Addrey
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILLE PREPERENCE: 2021-01-24
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILLING DATE: 1997-10-17
PRIOR FILLING DATE: 1997-11-03
PRIOR FILLING DATE: 1997-11-13
PRIOR FILLING DATE: 1998-03-10
PRIOR FILLING DATE: 1998-03-11
PRIOR PRILING DATE: 1998-03-11
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PRIOR PILLING DATE: 1998-03-13
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PRIOR FILING DATE: 1938-03-20
PRIOR PELLING DATE: 1938-03-20
PRIOR APPLICATION NUMBER: 60/07924
PRIOR PELLING DATE: 1938-03-26
PRIOR APPLICATION NUMBER: 60/07964
PRIOR PILLING DATE: 1938-03-26
PRIOR PELLING DATE: 1938-03-26
PRIOR PELLING DATE: 1938-03-27
PRIOR PELLING DATE: 1938-03-37
PRIOR PELLING DATE: 1938-03-31
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Filvaroff, Ellen
Fong, Sheman
Gao, Wat-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddward, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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; Publication No. US20030004102A1 ; GENERAL INFORMATION: ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Baker Kevin P. ; APPLICANT: Beter Kevin P. ; APPLICANT: Beterin, David ; APPLICANT: Eaton, Dan ; APPLICANT: Eaton, Dan ; APPLICANT: Farrara, Napoleon ; APPLICANT: Fong, Sherman ; APPLICANT: Fong, Sherman ; APPLICANT: Gerber, Hanspeter ; APPLICANT: Gerber, Hanspeter	Gerritser Goddard, Goddwrd, Goddwrd, Gurney, Hillan, Kljavin, Kuo, Soph Napier, Napier, Pan, Jame Pan, Jame	APPLICANT: Stewart, Timochy A.  APPLICANT: Timas, Daniel  APPLICANT: Williams, Daniel  APPLICANT: Williams, Daniel  APPLICANT: Wood, William I.  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  TITLE OF INVENTION: Acids Encoding the Same  FILE REFERENCE: P2630PlC7  CURRENT APPLICATION NUMBER: US/09/978,189  PRIOR FILING DATE: 2001-10.15  PRIOR PILING DATE: 2001-07-30  PRIOR PILING DATE: AND MARRER PAPLICATION NUMBER: 09/918585	PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/66429 PRIOR PILING DATE: 1997-11-03 PRIOR PILING DATE: 1997-11-03 PRIOR APPLICATION NUMBER: 60/66531 PRIOR PILING DATE: 1997-11-13 PRIOR PILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-21 PRIOR FILING DATE: 1998-03-10 PRIOR FILING DATE: 1998-03-11 PRIOR FILING DATE: 1998-03-11 PRIOR FILING DATE: 1998-03-11 PRIOR FILING DATE: 1998-03-11 PRIOR PLING DATE: 1998-03-11	APPLICATION NUMBER: PILING DATE: 1998-03 APPLICATION NUMBER: PILING DATE: 1998-03 APPLICATION NUMBER: PILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-03 APPLICATION NUMBER:	FILING DATE: 1998-03-25 APPLICATION UNDREK: 60 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-37 APPLICATION NUMBER: 60/
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GENERAL INPORMATION:
APPLICANT: ASHKenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bestein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
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Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBERS: P2630PLC15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-04-01
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PLICATION NUMBER: 60/081070
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PPLICATION NUMBER: 60/081195
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ICATION NUMBER: 60/081203
VG DATE: 1998-04-09
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PLICATION NUMBER: 60/081817
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PPLICATION NUMBER: 60/081838
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PLICATION NUMBER: 60/082568
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DATE: 1998-04-28
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PPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/084366
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URRENT APPLICATION NUMBER: US/09/978,191A
RIOR RILING DATE: 2001-10-15
RIOR APPLICATION NUMBER: 09/918585
RIOR PELING DATE: 2001-07-30
RIOR FILING DATE: 1907-10-17
RIOR FILING DATE: 1997-10-17
RIOR FILING NUMBER: 60/062250
RIOR FILING NUMBER: 60/064249
                                              Christopher
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APPLICATION NUMBER: 60/079656
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ILING DATE: 1998-03-10
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ION NUMBER: 60/079294
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IG DATE: 1998-03-27
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APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
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                                                                                                                                                                                                                                                                                                                                       Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                  neiton, David L.
tewart, Timothy A
                                                                                                                                                                                                                 Nicholas F
                                                                                                                                                                                                                                             Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998-03-20
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                                                                                                  Hillan, Kenneth
                                                                                                                           Ivar J
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Goddard, Audrey
                                                                                                                                                                       Wapier, Mary A.
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                         Godowski, Paul
Grimaldi, J. Cl
                                                                                                                    Kljavin, Ivar
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                   Tumas, Daniel
                                                                                                                                                                                              , James
                                                                                                                                                                                                                                                                                              Stewart,
                                                                                                                                                                                                                        Paoni,
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70.2%; Score 1078.8;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches
R FILING DATE: 1998-05-05

R APPLICATION NUMBER: 60/084414

R APPLICATION NUMBER: 60/084441

R FILING DATE: 1998-05-06

R RELING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084637

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084640

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084508

R FILING DATE: 1998-05-07
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R APPLICATION NUMBER: 60/084643
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60/085338
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R APPLICATION DATE: 1998-05-13
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R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/085700
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/085689
R FILING DATE: 1998-05-15
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R FILING DATE: 1998-05-15
R PAPLICATION NUMBER: 60/085580
R PILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/085573
R APPLICATION NUMBER: 60/08578
R APPLICATION NUMBER: 60/08578
R APPLICATION NUMBER: 60/085784
R FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/079923
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PPLICATION NUMBER: 60/080105
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PPLICATION NUMBER: 60/080194
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FILING DATE: 1998-04-22
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1546 CAAGCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1605
                                                                                                       1465 GGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAA 1524
                                                                                                                                                          1606 GCCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAGA 1665
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APPLICANT: Wood, William I.
LITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
LITTLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2639PIGT: US/09/978,403A
CURRENT APPLICATION UNBER: US/09/978,403A
CURRENT FILING PAIR: 2002-03-19
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Publication No. US20030050240A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/064249
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APPLICATION NUMBER: 60/065311
APPLICATION NUMBER: 60/065314
APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/077450
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PLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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FILING DATE: 1998-03-12
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tewart, Timothy A.
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Gerritsen, Mary E
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Filvaroff, Ellen
Fong, Sherman
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Desnoyers, Luc
Eaton, Dan
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10, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, Davi
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Oy 1 ATGCTACTGCCACTGCTGCTGCTGGGGGGGTCCCAGGCTATGGATGG	OY 121 TGCTCTTTCCCGACAGGACTGGACAGGGCTACCCCAGCTTATGGCTACTGG 180	Oy 181 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 240	Oy 241 GAGGTGGAAATGAGCACCCGGGGCCCATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 300	OY 301 IGCTCCTIGGTGATCAGGACGCGCAGATGCAGGATGAGTCACTACTTTCGGGTG 360	QY         361 GAGAGAAGTATGTGAGATATAATTTCATGAACGATGGTTCTTTCT	QY 421 GCCCTGACTCAGAGCCTGATGTCTACATCCCGGAGACC	Qy         460	486 CAICTGIGGGTTTAACTGGGCCTTTGAGAATGTCCACCCCTTCTTTCT	546 646	606	642	Qy 702 GGCCTATGCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCC752	Qy 753AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGCT 804	QY 805 CTGGAAAACCTTGGGAACGCCACGTCTCCCCAGTACTGGAGGCCAAAGCCTGTGCCTG 864	Qy         965 GTCTGTGTCACACACAGAGCCCCCCAGCCAGGCTCAGGCTCAGAGGGGACAGGTT         924	925 CTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCTCGGGTTCAAGTGGAG	Db 1066 CTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTGGGGTTCAAGTGGAG 1125 QY 985 CACGAAGGAGAAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCACTGGGCTCCTCTCTC 1044
FILING DATE: 1998-04 APPLICATION NUMBER: FILING DATE: 1998-04 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-04	APPLICATION NUMBER: 60/08339; FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/08349 FILING DATE: 1998-04-29	APPLICATION NUMBER: 60/08349 FILING DATE: 1938-04-29 APPLICATION NUMBER: 60/08349 FILING DATE: 1998-04-29	; PRIOR APPLICATION NUMBER: 60/083545 ; PRIOR FILING DATE: 1998-04-29 ; PRIOR APPLICATION NUMBER: 60/083554 ; PRIOR FILING DATE: 1998-04-29	; PRIOR APPLICATION NUMBER: 60/083558 ; PRIOR FILING DATE: 1998-04-29 ; PRIOR APPLICATION NUMBER: 60/083559 ; PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083500 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-30 PRIOR FILING DATE: 1998-04-30	; PRIOR APPLICATION NUMBER: 60/084366 ; PRIOR FILING DATE: 1998-05-05 ; PRIOR APPLICATION NUMBER: 60/084414 ; PRIOR FILING DATE: 1998-05-06	; PRIOR APPLICATION NUMBER: 60/084441 ; PRIOR FILING DATE: 1998-05-06 ; PRIOR APPLICATION NUMBER: 60/084637	FRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-06-07 PRIOR PETING DATE: 1998-06-07	PRIOR APPLICATION NUMBER: 60/084598  PRIOR FILING DATE: 1998-05-07  PRIOR PELLING DATE: 1998-05-07  PRIOR PELLING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084627  PRIOR FILING DATE: 1998-05-07  PRIOR FILING DATE: 1998-05-07  PRIOR FILING DATE: 1998-05-07	APPLICATION NUMBER: 60/08 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/08 FILING DATE: 1998-05-13	PRIOR APPLICATION NUMBER: 60/085323 PRIOR FILING DATE: 1998-05-13 PRIOR PILING DATE: 1998-05-15 PRIOR PILING DATE: 1998-05-15	; PRIOR APPLICATION NUMBER: 60/085700 ; PRIOR FILING DATE: 1998-05-15 ; PRIOR APPLICATION NUMBER: 60/085689 ; PRIOR FILING DATE: 1998-05-15	APPLICATION NUMBER: FILING DATE: 1998-05 APPLICATION NUMBER: FILING DATE: 1998-05	APPLICATION NUMBER: FILING DATE: 1998-05 APPLICATION NUMBER: FILING DATE: 1998-05	80	Similarity 81.4%; Pred. No. 0; 9; Conservative 0; Mismatches 207; Indels 96

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Acids Encoding the Same
                  FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
                                                                               PRIOR APPLICATION NUMBER: 09/918585
PRIOR PELING DATE: 2001-07-30
PRIOR PEPLICATION NUMBER: 60/062250
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR PELING DATE: 1997-11-21
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                                                                                                               1186 AGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGCCATTCTCCAACGCGTTT
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Gurney, Austin L.
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Roy, Margaret Ann
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ilvaroff, Ellen
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PRIOR APPLICATION WURBER: 60/081195
PRIOR APPLICATION WURBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-09
PRIOR PAPLICATION WURBER: 60/081229
PRIOR PAPLICATION WURBER: 60/081269
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Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 207; Indels PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/08533
PRIOR PELING DATE: 1998-05-13
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Sequence 258, Application US/0999933A Publication No. US20030054405A1 GENERAL INFORMATION:

APPLICANT: Askersiz, Avi

APPLICANT: Baker Kavin P.

APPLICANT: Baker Kavin P.

APPLICANT: Beleve Kavin P.

APPLICANT: Beleve Kavin P.

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APPLICANT: Glow Feel, Manger E.

APPLICANT: Glow Feel, Ambrew C.

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PRETING DATE: 1998-03-27

PRAPLICATION NUMBER: 60/079920

PRILING DATE: 1998-03-30

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PRIOR APPLICATION NUMBER: 60/08269
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Gao, Wei-Qiang
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APPLICANT: Baker Kevin P
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION UNDER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity 81.4%;
Matches 1329; Conservative (
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PRIOR PILLING DATE: 1998-04-22
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R FILING DATE: 1998-03-27
R PAPLICATION NUMBER: 60/07969
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R APPLICATION NUMBER: 60/080194

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PRIOR PILL
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'S sequence 258, Application US/09918585A
'Publication No. US20030060406A1
'GENERAL INFORMATION:
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Flvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
1525 GTCAAGTTCCAA 1536
                                                                     1666 GrcaaGrrccaa 1677
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APPLICANT: Baker Kevin P.
APPLICANT: Betsein, David
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Query Match 70.2%; Score 1078.8; DB 10; Length 2764; Best Local Similarity 81.4%; Pred. No. 0; Matches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps

61 ITCTGGATACGAGTGCAGGGTCAGTGCTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120

1186

1065 AGCCTCTCCGTGCACTATAAGAAGGACTCATCTCAACGCATTCTCCAATGGAGCGTTT 1104 420 645 CTGGAAAACCTTGGGAACGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 1005 180 300 360 465 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 165 405 605 885 864 701 804 GAGGTGGAATGAGCACCCGGGGCCGATTCCACTCACTGGGGATCCCGCCAAGGGGAAC 346 IGCICCTIGGTGAGACGCGCAGAIGCAGGAGAGAGAGAGAGAGAGAGACTACTITCGGGTG 406 GAGAGAGGAAGCTATGTGACATATATATTCATGAACGATGGGTTCTTCTAAAAGTAAGA 865 GTCTGTGTCACACACCAGCCCCCCAGCCAGACTGACCCAGAGGGAACAGTT
1006 GTCTGTGTCACACACACCAGCCCCCCAGCCCAGAGCGACAGAGTT TGCTCTTTCTCCTACCCCCGGACAGGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCCACAAACCACCAGAGTCGA TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGGAGTCGA 286 GAGGIGGAAATGAGCACCCGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC TGCTCCTTGGTGATCAGAGGCGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 526 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCC 586 AGAGACCTTGTTATCAGGATTTCACGTGACACACGCCCAGCCCTGGAGCCCCCAGGCCCCAG GGCTGCCCTCTCCCAAGGAACCAAACCAACGACCTCCCCACTTCTCAGTGCTCAGCTT 606 CACGCCCAGGACCCCAGGACCACAC------GACACCGACCTCAC carcocrassaccocrassaccocrassaccrassaccoccassarsaasccrassaarraa desciectacacións de desciencia de desciencia de desciencia de de desciencia de descienc -----AGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC TCTGTGCAGTATCCTCCAGAGAACCTGAGAGGAGGATGGTTTCCCAAGCAAACAGGACAGTC CTGGAAAACCTTGGGAACGCCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 646 GGAAATGTCCCATACCTGGAAGCCCAAAAAGCCCAGTTCCTGCGCCTCCTGTGCTGCT CTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGGGCACAGAGGACCGTCCGACTCCGTGT CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG CTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGGAGCTGCTCGGGGTTCAAGTGGAG CACGAAGGAGATTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGGACACGACATCTCTC GACAGCCACCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC GGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACACACGCC-----GCCCTGACTCAGAAGCCTGATGTCTACATCCCCCGAGACC-166 421 ( 90T 226 241 946 181 1045 301 466 486 642 994 1066 546 206 702 826 753 805 925 985 ò G \$ B \$ 8 8 8 8 8 8 8 දු දු q  $\dot{\delta}$ P ò 엄 g S g 셤 ò ઠે  $\dot{\delta}$ g ठे 엄 엄 8 ä q ò g 8

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qq	1246	CTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGGCCCTGATCATCATGAAGATT 1305
ò	1165	CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGGACAGGACG 1224
qu	1306	CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCCGGCACGCAC
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qq	1426	AAAGCCACACACAAACAGTCCTCGGACCCCTCCTCCACAGGTGCTCCTCCCCCAGAATCA 1485
ζ	1345	AAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACT 1404
qq	1486	AAGAAGAACAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCAT 1545
δ	1405	CAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCA 1464
QQ	1546	CAAGCCCCAGAATCCCAGGAGAGCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCCA 1605
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δλ	1525	GTCAAGTTCCAA 1536
ДD	1666	GTCAAGTTCCAA 1677

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 1011)

2. (Dases 1 to 1011)

3. Li, W.B.; Gruber, C., Jessee J. and Polayes, D.

4. Full-length cDNA libraries and normalization

5. Low May 5, 2003 this sequence version replaced gi:30373021.

6. On May 5, 2003 this sequence version replaced gi:30373021.

7. Contact: Genoscope

6. Genoscope - Centre National de Sequencage

8. P191 91006 ENX cedex - France

8. Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster

Homo sapiens (human) Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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| /clote="tst strand cDNA was primed with a Not1-cligo(dT)
| primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CSOAIO25BB12QP1&c=9384.r. Location/Qualifiers

9384.r

FEATURES

4.

Gaps

51;

36.8%; Score 565.4; DB 5; Length 1011; llarity 77.7%; Pred. No. 2.1e-141; Conservative 4; Mismatches 160; Indels 51;

Query Match Best Local Similarity Matches 750; Conserv

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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12357 row: o column: 04
High quality sequence stop: 725.
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35.0%; Score 537.2; DB 4;
al Similarity 86.0%; Pred. No. 9.2e-134;
607; Conservative 0; Mismatches 98;
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/db_xref="taxon:9606"
/clone="IMAGE:5587803"
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                                                                                      BM544297.1 GI:18775435
                                                                                                                                                                                      Homo sapiens (human)
mRNA sequence
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EM544297 1099 bp mRNA linear EST 20-FEB-2002 AGENCOURT\_6490592 NIH\_MGC\_125 Homo sapiens CDNA clone IMAGE:5587803

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BX470328 514 bp mRNA linear EST 04-SEP-2003
DKF2p779N169 r1 779 (synonym: hnccl) Homo sapiens cDNA clone
DKF2p779N169-5', mRNA sequence.
BX470328
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemannGdkfz' heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZP): Ressourcenzentrum, Heubnerweg 6, 14059
Blease contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                            GTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACAAACAGTC-- 1303
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/note="Vector: pSportl_Sfi; Site_l: SfilA; Site_2: SfilB"
                                           186 ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACACCACGATCCTGGATTACATCAATGTG
                                                                                                                                                                                                          181 GCAGATACCCCAAGGCCCAGGTTCTCCCGGCACACGATGCTGGATTACATCAAGATGTG
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/lab_host="DH10B"
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                            CGGGGGCTGCCCTCCTCCCAAGGAACCAAACCAACGACCTCCCACTTCTCAGTGCTCA
                                                                      cecngaencasaasecenganeneneneeneeasecengaasecegggeggeggeggeggegg
                                                                                                                                                                                                              CGGTCATCTGTGTGTTTAACTGGGCTTTCAAGAAATGTCCAGCCCCTTCTTCTCCTGGA
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Similar to GenBank entry AF311905 AF311905 Homo sapiens sialic
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/201
Plate: MMSP0040 row: D column: 05.
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Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
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MMSP0040 D05 MMSP Macaca mulatta cDNA, mRNA sequence.
CB554607
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31.1%; Score 478; DB 6; Length 667;
Best Local Similarity 94.8%; Pred. No. 8.3e-118;
Matches 506; Conservative 0; Mismatches 25; Indels
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Contact: Holzman T
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Box 358070, Seattle, WA 98195-8070,
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington Adv.
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db_xref="taxon:9544"

sex="male"

cell_type="monocytes"

dev_grage="adult"

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note="Crgan: spleen"
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1 (Dases 1 to 1464)

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

Ontational Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapber:@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLAM12357 row: m column: 22
High quality sequence start: 87
High quality sequence stop: 427.
                                                                                                 183 TGCTCTTTCTCCTACCCCCGACAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG
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Score 448.8; DB 5;
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mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5587773"
/lab_host="DH10B"
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Owery Match
Best Local Similarity 99.6%;
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1745)
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                                                                                                     Contact: Addition Straughts, First.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: Limal 364 row: o column: 15

High quality sequence start: 64

High quality sequence stop: 538.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nature 420, 563-573 (2002)

E (bases 1 to 2017)

E (bases 1 to 2017)

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission
Submitted (20-UIL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Li W. Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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(human)
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse Lissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/
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SRMSTQRTVELRVASMSPRSLALSTFHDWSVPDLHENPSHLEVQGGSLRLLCTABSQ
PPATLSWYLBDQVLSMSSPVGSRTLALBLPWYKAGDSGHYTCQABRAGSQQALRLLCTABSQ
VLYPPODLRVTVSQANRTVLEILRNAISLPWTGGGSLCLVCYTYSNPPANVSWAWTG
TLIPTDSSEBPGVLEDPUVGREHGEFTCAAQNPLGAQRISLSUHYPPPQMSSPSCW
FACHHCNCSSRAWAPSLWRTGGGLLEGNSNASFTVTFSSLGSWYNSSLELQEI
GPSLMLSCESWNTHGAQTTSVLLLFDKDSATAFSKGAVLGFGITALLALCLIVVIVKT
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147. ..2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MSLLLFLLSFLLDGPQGQMESYFLQVQRIVKAQEGLCIFVPCSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOKKGTOEEPSRPKLSRGSTILDYINVVPKTRSLARNWKAEPDAPSRSSPLDTHFPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 TTAGAATGGGAAGCCCGAGGCGCTTCCAGCTCTTGGGGGGATATCTCTAAAAAAGAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; putative
weakly similar to SIALIC ACID-BINDING LECTIN [Homo
sapiens] (SPTR]QS6RL6, evidence: FASTY, 61.6%1D,
84.6%length, match=1719)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 338; DB 3; Length 20 Pred. No. 8.6e-80; Mismatches 340; Indels
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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ilarity 61.8%;
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Best Local Similarity
Matches 658; Conserv
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2004
sapiens
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Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
--ccaaggaaaacagcgcagccttcaaaatcctgcaaaacacctcgtcctcctcctcctc
                                                                                 GGGCTCCCAGCACGTCTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAAC
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                                                                                                                                               GCTGCCTCGGGTTCAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACT
                                                                                                                                                                                                               1039 GCTGCCTCAAGTAGGGTCTGCAGAAGAAGAAGATTTCACCTGCCGTGCTCAGCATCCTCT
                                                                                                                                                                                                                                                                                                               1083 GGCATTCTCCAATGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Pred. No. 3.1e-76;
0; Mismatches 392
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21.1%;
Best Local Similarity 60.0%;
Matches 714; Conservative 0
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HTC; CNSLT CDNA.
Homo sapiens (human)
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 - Web : www.genoscope.cns.fr)
lst strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 2.8e-76;
0; Mismatches 392;
                                                                                                              1. 1313

/organism="Homo sapiens"

/db_rref="taxon:9606"

/db_rref="taxon:9606"

/clone="csobpouly118"

/tissue type="Placenta"

/plasmid="pcMVSPORT_6"
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		243 GGTGGAAATGAGCCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACTG 302	GAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	GGTGTTCGTGTGTTTAACTGGCTTTTGAGGAATGTCCACCCCTTCTTTCT	673 GTCAGCTGCCCCCAGGACCCCCAGGACCACCCCAGTGCTCGC 726  603 CTTCAGGCCCAGGACCACGACACGACCTCACCAGTGCTCTCCAG 662  1	787 AGCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	783 TTCCCAAGGAACAGGACAGTCTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACT 842 	843 GGAGGCCAAAGCCTGTGCTGTGTCACACAGCCCCCCCAGCCAG	903 CTGGACCCAGAGGGACAGGTTCTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGA 962	GCTGCCTCAAGTAGGGTCTGCAGAAGAAGAGTTTCACCTGCGTGCTCAGCATCTCT 10 GGGCTCCCAGCACGTCTCTCAGCCTCTCCGTGCATAAGAAGAGACATCTCT 10	1099 GGGCTCCCTGCAAATCTCTCTGAGTCTCTTTGTGCAAACCAGAAGGCAGGGCTGG 1158 1083 GGCATTCTCCAATGGAGGTTTCTGGGAATCGGCATCACGGCTCTTTTCCTCTGCCT 1142

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

LOCUS

RESULT 11 BC030222

ACCESSION

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/tissue type="Blood, adult leukocytes"
/clone lib="NIH MGC_118"
/lab_host="DH10B"
                                                                                       /note="Vector: pCMV-SPORT6"
/clone="IMAGE:5211307"
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Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: Gagbbs-ragmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing by: National Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web sites http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Quuan,X., Guta,J., Haghighi,P.,
Manduro,D.L., Maskerlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,D.L., Maskerlins,S., S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.U., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 49 Row: j Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1714 bp mRNA linear HTC 04-MAR-2003 HOMO sapiens, Similar to sialic acid binding 1g-like lectin 11, EC030222
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                              352 gerectrogranchandacecechangagarandarandaratrogrander
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/db_xref="taxon:9606"
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Strausberg, R.
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Bukaryota, Mamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

The Cosses 1 to 565

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.,
Thuman Unigenesset - RZPD3

L Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD, IMAGP958K04115.

RZPDILB; I.M.A.G.E. CDNA Clone Collection;
Human Unigenesset - RZPD3 (RZPDILB) No.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7libNo=972 Contact: Ina Rolfs
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BX283650 NIH MGC 48 Homo sapiens cDNA clone IMAGp958K041152 ;
IMAGE:4297851, mRNA sequence.
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                                                      Gaps
                                                      4.
     Length
                                                      Indels
Score 320.6; DB 3;
Pred. No. 4.2e-75;
0; Mismatches 89;
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AK036698
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany 1911 +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: pCMV-M13u, Primer Sequence: CGTTGTAAAACGACGGCCAGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 870 TGTCACACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGGACACAGGTTCTGAG 929
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGTATCCTCCAGAGAACCTGAGAGTGATGCTTTCCCAAGCAACAAGGACAGTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   810 AAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 CCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990 AGGAGAGITCACCIGCCACGCICGCACCCACTGGGCICCCAGCACGICICICICAGCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construct 20.0%; Score 307.2; DB 5; Length 505; Best Local Similarity 99.0%; Pred. No. 1.3e-71; Matches 309; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF663289.1 GI:11937171
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AUTHORS
TITLE
JOURNAL
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Directionally cloned into EcoRI/Knol sites using the following S' adaptor: GGGACGAG(G). Size-selected >SoObp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkelsy) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1049
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                           DNA Sequencing by: Incyte Genomics, inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1152 row: k column: 04
High quality sequence stop: 661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 IGTCACACACACAGCGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       750 GCCAGATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AAACCTTGGGAACGGCACGTCTCCCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTG
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Contact: Robert Strausberg, Ph.D.
Famal: gapbs-remail.ini.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.0%; Score 307.2; DB 2; Length 99.0%; Pred. No. 1.5e-71; iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/tissue_type="bone"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 AGAGGA---trrigagagarrongrific---aaggagagricaggcracaagrogaagcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGCCTGTGCATCTCTGTGCCTTGC
                                                                                                                                                  /note="unnamed protein product; putative weakly similar to SIALIC ACID-BINDING LECTIN [Homo sapiens] (SPTR|Q96RL6, evidence: FASTY, 61.6%ID, 84.6%length, match=1719)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 301.6; DB 3;
Pred. No. 7.2e-70;
0; Mismatches 219;
              clone="9830164H23"
                                                                                  /clone_lib="RIKEN | /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                           1919. .3924
'note="putative"
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al Similarity 67.3%;
475; Conservative
                                     /sex="male
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Best Local
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                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Riki nitegrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@ger.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome based on functional annotation 660,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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|strain="C57BL/6J"
|db_xref="FANTOM_DB:9830164H23"
                      Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/lab host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_106"
/note="Organ: Blood; Vector: pOTB7; Site_1: Xho1; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xho1 sites using the following S, adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT_6595995 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5484658
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLCM2014 row: e column: 11
High quality sequence stop: 609.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches 272; Indels 10;
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Tissue Procurement: Dr. Daniel McVicar,
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/db_xref="taxon:9606"
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US-09-937-636-2 1917 1 atgctactgccactgctgct.....atgcagaagtcaagttccaa 1917 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4526729 seqs, 23644849745 residues Total number of hits satisfying chosen parameters: Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 BD011516	
LOCUS DEFINITION	BD011516 31-JAN-2002 Sialoadhesin family 4(SAF-4) cDNA.
ACCESSION VERSION	BD011516 BD011516.1 GI:18639889
KEYWORDS	JP 2001502359-A/1.
SOURCE	Homo sabiens (numan) Homo sabiens
	Mammalia; Eutheria; Primates; Cacarrnin; Hominidae; Homo. 1 (1922, 1920, 2000)
REFERENCE	I (bases I to 3099) Kikly.K.K. and Miller, C.L.E.
TITLE	
JOURNAL	Patent: JP 2001502359-A 1 20-FEB-2001;
	THEFT
COMMENT	OS Homo sapiens (human) PN JP 2001502359-A/1
	PD 20-FEB-2001
	27-MAY-1998 JP 199
	PI KRISTINE KAY KIKLY, CONNIE LYNN ERICKSON MILLER PC
	A61K38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705, PC
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ORIGIN	
Query Match	oh 100.0%; Score 1917; DB.6; Length 3099;
Best Local Sig Matches 1917;	nitarity 100.0%; Conservative 0;

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ge Page 2	1191   AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGCGCCCTCCTCGTCCTCGGGAGCTGAG   1200   1191   AGCCTCTCCGTGCACTCTCCCCGAAGCTGCTGGGGCCCTCTCTCT	BD011517  BD0115
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1261 GGGGAGGAGCTGCTGGAGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCCAGGTCA 1320
                                                                                                                                GAGGIGGAAATGAGCACCCGGGGCCGAIICCAGCICACIGGGGAICCCGCCAAGGGGAAC 300
                                         238 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAAGGTGGA
                                                                                                                                                                         GACAGCCAGCCCCTGCCACACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838 GGGGGGTACACCTGCCGAGCGGAGCACACGCTTGGCTCCCAGCAGCGAGCCCTGGACCTC
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   TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA
                                                                                                                                                                                                                                                                TECTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTTCGGGTG
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PI FAUL A MOORE,YING FEI WEL,JOHN M GREENE
PC CI2N15/09,A61K31/7088,A61K35/76,A61K38/00,A61K39/39/
PC 395,A61K48/00,
PC 395,A61K48/00,
PC 395,A61F7/00,A61P7/06,A61P9/10,A61P11/06,A61P17/02,A61P17/PC
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Bukaryota.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2295)

Ni,J., Ruben,S., M., Olsen,H.S., Young,P.E., Kenny,J.J., Moore,P.A.,

Wei,Y.F. and Greene,J.M.

Patent: JP 2002330066-4

HJ7-SEP-2002;

HUMAN GENOME SCIENCES INC
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JP 2002530062-A/14
17-SEP-2000
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Key Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches
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1. 2295
7. Crganism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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12 human secreted proteins.
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JP 2002530062-A/14.
Homo sapiens (human)
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1 (bases 1 to 2126)
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Biochem. Biophys. Res. Commun. 296, 355-362 (2002)
Z. (bases 1 to 2126)
Kitzig, F., Alvarez-Errico, D., Sayos, J. and Lopez-Botet, M. Direct Submission
Submitted (17-ARR-201) Immunology, Universitat Pompeu Fabra (CEXS), Dr. Aiguader No. 80, Barcelona 08003, Spain
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tt="sialic acid binding immunoglobulin-like lectin
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1.6%; Pred. No. 0;
ve 0; Mismatches 2; Indels 174; Gaps
                                                                                                          "SIGLEC10"
"Siglec-10"
SIGLECIO"
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Oy 1567 ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACA Db 1778 ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACA Oy 1627 GTCCCGACGCTCGCCCCTGGCTCAGAGCGAC Oy 1687 CGGACCCTTCCCACCAGGTCTCCCCCAG Oy 1747 TATCAGTTGCCCAGTTCCCCAGACCCAG Oy 1747 TATCAGTTGCCCAGTTCCCAGAACCA Oy 1747 TATCAGTTGCCCAGTTTCCCAGAACCAT Oy 1747 TATCAGTTGCCCAGTTTCCCAGAACCAT Oy 1747 TATCAGTTGCCCAGTTTCCCAGAACCAT Oy 1747 TATCAGTTGCCCAGTTTCCCAGAACCCAATCAT Oy 1807 AGCCAAGAGGAGTCCATTTTTCCAGAACCCAAATCAT Oy 1807 AGCCAAGAGGAGTCCATTTTTTTTTTTTTTTTTTTTTTT	RESULT 10 AX365518 LOCUS Sequence 3 from Patent W00208257. ACCESSION AX365518 VERSION AX365518 AX365518 AX365518 I GI:18697087 KEYWORDS Homo sapiens (human) CRGANISM BUKATYOTA: Metaza; Chordata; Crania Mammalia; Butheria; Primates; Catarr Mach Patent: W0 0208257. AUTILE JOURNAL BRISTOL-WYERS SQUIBS COMPANY (US) FEATURES OURCE AUTICLE JOURNAL BRISTOL-WYERS SQUIBS COMPANY (US) FEATURES OURCE AUTICLE JOURNAL BRISTOL-WYERS SQUIBS COMPANY (US) FEATURES AUTICLEAGUAGACCAGACCAGACCAGACCAGACCAGACCAGACCA	
638 AGCTTCACGCCCAGACCCCAGACCACCGACCTCCCCTGCCATGTGGACTTCTCC 697  487 AGAAAGGGTGTGACGCACAGAGGACCGTCCGTGTGGCCTATGCCCCCAGAGAC 546  698 AGAAAGGGTGTACAGACACAGAGCCCTCCGTGTGGCCTATGCCCCCAGAGAC 757  547 CTTGTTATCAGCATTTCACGTACACACCCCCAGCTGTGGCCTATGCCCCCAGAGAAT 606  758 CTTGTTATCAGCATTTCACGTGACACACCCCCAGCCCCAGGGAAT 817  607 GTCCCATACCTGGAACACACACACCCCCAGCCCCAGGGAAT 817  607 GTCCCATACCTGGAACACACACACACACCCCTGGAGCCCCAGGGAAT 817  607 GTCCCATACCTGGAACCCCAAAAAGGCCAGCCCCTGCAGCCCCAGGGAAT 817  607 GTCCCATACCTGGAACCCCAAAAAGGCCAGCCCCTGCAGCCCCAGGCCCAGGAAT 817  607 GTCCCATACCTGGAACCCCAAAAAGGCCAGCCCCTGCAGCCCCAGCCCCAGGAAT 817  608 GTCCCATACCTGGAACACAGACACACACACACACACACCCTCTGTGCTGCTGACAGC 817  609 GTCCCATACCTGGAACACACACACACACACACACACACAC		

linear PAT 15-FEB-2002 1897 2017 AGAATCAAAGAAGAACCAGAAAAAGCAG 1746 1806 1837 1686 538 357 AACACGCCAGCCCTGGAGCCCCAGCCCC 598 iata; Vertebrata; Euteleostomi; rrhini; Hominidae; Homo. STCCTGCAGAACAGAGTCCTCTCCTCGT ACCGTCCGACTCCGTGGCCTATGCCC CAGCACGATTCCTGGATTACATCAATGTG ATCCACTCAAGCCCCAGAATCCCAGGAG CTTCCCAGGCGTCAGACCCAGGCCTGAG SCCAGTTCCTGCGCTCTCTGTGCTG 0; Gaps GCAGAAGTCAAGTTCCAA 2128 GCAGAAGTCAAGTTCCAA 1917 DB 6; Length 2823; 1; Indels DNA

	11 16 16 TION ION N	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Longphre, M., Chang, H. and Whitney, G. TITLE Novel sigleds and uses thereof JOURNAL Patent: WO 0208257A 1 31-7002;	FEATURES LOCATION (US) FEATURES 12565 12565 // Organism="Homo sapiens"."	ol_type="unassigned DNA b_xref="taxon:9606"	Query Match 69.7%; Score 1337; DB 6; Length 2565; Best Local.Similarity 85.1%; Pred. No. 8.2e-282; Matches 1632; Conservative 0; Mismatches 0; Indels 285; Gaps 1;	Qy 1 ATGCTACTGCCACTGCTGCTGCTGCTGGCGGGCGGGCCCCAGGCTATGGATGG	Qy 61 TICTGGATACGAGTGCAGGAGTCAGTGATGCTGCCGGAGGCCTGTGCATCTCTGTGCCC 120	OY 121 IGCTCTTTCTCCTACCCCGACAAGACTGGACGGGTCTACCCCAGCTTATGGCTACTGG 180  Db 249 IGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 308	OY 181 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACGAGTCGA 240  Db 309 TTCAAAGCAGTGACAACCAAGGGTGCTCCTGTGGCCACAAACCACGAGTCGA 368	Qy 241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTGACTGGGGATCCCGCCAAGGGGAAC 300  16	QY 301 TGCTCCTTGGTGATCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360	OY 361 GAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	A21 GRGCTCAGCTTCACGCCCAGACCCCAGACCCCACACCCCACCTCACCTGCCATGTGGAC 480	Qy         481 TTCTCCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGTGTGGCCTATGCCCCC         540           Db         609 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGTGTGGCCTATGCCCCC         668	Qy 541 AGAGACCTTGTTATCAGATTTCAGGGGAACCGCCAGCCCTGGAGCCCCAGCCCAGCCCCAG 600
Qy         719         CCCATCCCTGGGGCCCTAGGACCCCTGGGGCTGGAGGTGAAGGCTGGGGGTT         778           Db         538         CCCATCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGAGGGTT         597            Qy         779         CAGGGGCTACACCTGCCGAGCGAGAACAGGCTTGGCTCCCAGCAGGAGGCCTGGACC         838            Db         598         CAGGGGCTACACCTGCCGAGCGAGAACAGGCTTGGCTCCCAGCAGCGAGGCCTTGGACC         638	Qy         839 TCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGCTTTCCCAAGCAACAGGACA         898           Db         658 TCTCTGTGCAGTATCCTCCCAGAGAACCTGAGAGTGATGCTTTCCCAAGCAACAGGACA         717           Qy         899 TCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGCCTGTGCC         958           Db         718 TCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGCCTAAAGCCTGTGCC         777	Qy 959 TGGTCTGTGTCACACAGCAGCCCCCCAGCCAGGTGAGCTGGACCCAGAGGGGACAGG 1018 	QY 1019 TICTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGG 1078	Oy         1079 AGCACGAAGGAAGAATTCACCTGCCACCACCACCACCACCACCACCACCACCACCACCACCA	OY 1139 TCAGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCTG 1198	1199 AGGICTGCACTGCAGCTGCTCCTCCAGGCCAGCCCGGCCCCTCTCTGCGCTGGTGGC 1258	9 TTGGGGAGGAGCTGCTGGAGGGAACAGCAGGCAGACTCCTTCGAGGTCACCCCCAGCT	OY 1319 CAGCCGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGTCAGGCCTCA 1378	9 GGCTCCGCTGTGGAGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC	CGGCA	OY 1499 TCACGGCTCTTCTTTTCCTCTGCCCTGATCATCATGAAGATTCTACCGAAGAGA 1558	TTACA	9 TCAATGTGGTCCGACGGCTGGCCCCCTGGGTCAGAAGCGGAATCAGAAAGCCACCAA 	9 ACAGTOCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGA 	739 AAAAGCAGTATCAGTTGCCCAGTTTCCCAAAACCAAATCACCACTACACAAAT 1	1558 AAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAAT 1617 1799 CCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCA 1858

GGGGGGGCCTGCAGCTGCTCCTCCCAGGCCCGGCCCCTCTCTGGCGTCGTCGTCGTCGTCGTCGTC
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1740	1800	1860	, 	-0	2007	·				<del>_</del>	09	0 (	165	180	240	285	300	9	5 G	465
Oy 1681 AGTCCTCGGACCCCTCTTCCACCAGGGCGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA : Db 1524 AGTCCTCGGACCCTCTTCCACGGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA :	OY 1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC :	1801 CAGAGAGCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGAGCAGGCAG	AAGGGCACCCAGGCGATTATGCAGAAGTCAAGTTCCAA 191		RESULT 12 CQ767791 LOCUS CQ767791 LOCUS CQ767791 DEFINITION Sequence 258 from Patent EP1386931. ACCESSION CQ767791 VERSION CQ767791 CQ767791 CQ767791.	Homo sapiens (human) Homo sapiens Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom	rd, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, n homologue	FEATURES Location/Qualifiers Location/Qualifiers 1.2764 /organism="Homo sapiens" /mol type="unassigned DNA" / ho type="unassigned DNA"	ORIGIN	Query Match 69.6%; Score 1333.8; DB 6; Length 2764; Best Local Similarity 85.0%; Pred. No. 4.1e-281; Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps	Qy 1 AIGCIACTGCCACTGCTGCTGCTCGCTGGCGGGGTCCCAGGCTATGGATGG	Db 46 AIGCIACIGCCACIGCIGCIGCCCCCGCIGCGGGCGGGTCCCAGGCIAIGGAIGGGAGA	Qy 61 ITCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGCCTGTGCATCTGTGTGCCCCCTGTGCCTGTGCCCCGAGGGCCTGTGCATCTGTGTGCCCCGAGGGCCTGTGCATCGTGCCCCCCCC	Oy 121 TGCTCTTTCTCCTACCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG  DA 166 POCTCTTTCTCCTACCCCCGACAAGACTGGAAGGGTCTACCCCAGCTTATGGCTACTGG	181	Db 226 TICAAAGCAGTGACAACCAAGGGTGCTCCTGTGGGCCACAACCACCAGAGTGGA	Qy 241 GAGGTGGAAATGAGCACCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGAAC	301	Db 346 IGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTC	Qy 361 GAGAGGAGGATGTGTGAGATATATTTCATGAACGATGGGTTCTTTCT

1261 ACGGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGAGACGG 132	Qy 1561 ACTCAGACAGAAACCCGAGGCCCAGGTTCTCCGGGCACACGATCCTGGATTACATC 1620	OY 1621 AATGTGGTCCCGACGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACCACCAAC 1680  1381 AATGTGGTCCCCACGGCTGGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACCAAAC 1440	1681 AGTCCTCGGACCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAGAAGAACAGAAAAAAAA	1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1741 AAGCAGTTATCAGTTGCCCAGTTTCCCAGAATCCATCATCATCATCAAGCCCCAGAATCATCATCAAGCCCCAGAATCATCATCAAGCCCCAGAATCATCATCAAGCCCCAGAATCATCATCAAGCCCCAGAATCATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCCAGAATCAAGCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCCAGAATCAAGCCCAGAATCAAGCCCCAGAAACAAGCCCCAGAAACAAGCCCCAGAAACAAGCCCCAGAAACAAGCCCAGAAACAAGCCCCAGAAACAAGCAAGCCCAGAAACAAGCCCAGAAACAAGCCCCAGAAACAAGCAAGAACAAGCAAGAACAAGCCCAGAAACAAGCCCAGAAACAAGCCCCAGAAACAAAAAA	1801 CAGGACAGCCAGGAGGACTCCATTATGCCAGGCTCAACTTCCCAGGCGTCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGAGAACCCAACTTATGCCACAGCTCAACTTCCCAGGCTCAGACCCAGACCCAGACTCATTATGCCACACTCACT	QY         1861         CTGAGGGCGGATGGCCAAGGGGAGGGGAGGTTCCAA 1917           DD         1621         CCTGAGGCCCGGATGCCCAAGGGCACCCAGGGGATTATGCAGAAGTTCAAGTTCCAA 1677	RESULT 13 AX376050 LOCUS AX3776050 LOCUS AX376050 L	AX376050 AX376050.1 GI:19170417	_	AUTHORS BARET, R.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.	ы	FEATURES LOCATION (MAILITEES SOURCE 1.2764 / Organism="Homo sapiens" / Mol_type="unassigned DNA"	/db_xret="taxon:9606" ORIGIN	core 1333.8; DB 6; Length 2764;	Matches 1630	Db 46 ATGCTACTGCTGCTGCTGCTGCTGGGGGGGCTGCTGGGGGTATGGATGG	OY 61 TICTGGATACGAGTGAGGGAGGGCCGGAGGGCCTGTGCATCCTGTGCCC 120		121 TGCTCTTTCTCCTACCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG	Db 166 IGCTCTITCTCCTACAAGACTGGACAAGAGTCTACCCCAGCTTATGGCTACTGG 225	226 TTCAAAGCAGTGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA
Oy 421 GTGCTCAGCTTCACGCCCAGACCCCACACCCACCCTCCCCTGCCATGTGGAC 480	1 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGC	41 AGAGACCTIGITATCAGCATTICAGGGGACACAGGCCAGCCCTGGAGCCCCAG	GAAANGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGGGGCTCCTTGTGCTGCTGCTGCTGCTGCTGCTG	1 GACAGCCAGCCCCTGCCACACTGAGCTCGGTCCTGCAGAACAGAGTCCT 		TACACCTGCCGAGCGGAGAACAG 	841 TCTGTGCAGTATCCTCCAGAGAGCTGAGAGTGTTCCCAAGCAAAAGGACAGTC 900 	901 CTGGAAACCTTGGGAACGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 960 	961 GTCTGTGTCACACAGCAGCCCCCAGCCAGGCTGACCTGGACCCAGAGGGACCAGGTT 1020 1006 GTCTGTGTCACACACCAGCAGCCCCAGCCAGGCTGAGCTGGACCCAGAGGGAACAGGTT 1065	1021 CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080	1081 CACGAAGGAGAGTTCACCTGCCACGCTCCACTGGGCTCCCAGCACGTCTCTCTC	1141 AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGTGAG 1200	1201 GGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGCCCCTCTCTGCGGCGGCTGGTT 1260	02	1 GGGGAGGAGCTGCTGGAGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 1	1202	1202 1201	1381 CTCCGCTGTGAGGCCTGGAACGTCCATGGGCCCCAGAGTGGATCCATCC	1202 1201	4r (	01 ACGGCTCTTCTTTTCCTCTGCCCTGGCCCTGATCATGAAGATTCTACGGAAGAGGC 156

Oy 1321 GCGGGCCCTGGGCCAACAGCTCCTGAG  Db 1202  Qy 1381 CTCCGCTGTGAGGCCTGGAACGTCCATGG  Db 1202	1501 1261 1561 1321 1621 1381	Oy 1681 AGTCCTCGGGCCCTCTTCCACCAGGTGC Db 1441 AGTCCTCGGACCCTCTCCACCAGGTGC Qy 1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGA Db 1501 AAGCAGTATCAGTTGCCCAGTTTCCCAGA Qy 1801 CAGGAGAGCCAAGAGGAGCTCCATTATGC Db 1561 CAGGAGAGCCAAGAGGAGCTCCATTATGC Db 1561 CAGGAGAGCCAAGAGGAGCTCCATTATGC	OY 1861 CTTGAGGCCGGATGCCCAAGGGCACCAAGGCACCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCCAAGGCCCCCAAGGCCCCCC		Xie, M.H., Yansura, D., Yi,S., Yu. Goddard, A., Wood, W.I. and Godow TITLE The Secreted Protein Discovery Effort to Identify Novel Human a Bioinformatics Assessment JOURNAL Genome Res. 1 (10), 2265-2270 PUBMED 2297309 Clark, H.F. (bases I to 2764)  REFERBNCE 2 (bases I to 2764)  AUTHUE Direct Submission JOURNAL Submitted (01-AUG-2003) Departmm Inc., I DNA Way, South San Fran Frances Inc., I DNA Way, South San Frances Inc., I DNA Way
241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGGTCACTGGGGATCCCGCCAAGGGGAAC 300 286 GAGGTGGAAATGAGCACCCGGGCGATTCCAGGTCACTGGGGATCCCGCCAAGGGGAAC 300 286 GAGGTGGAAATGAGCACCCGGGCGATTCCAGTGGGGTTCCCGCCAAGGGGAAC 345 301 TGCTCCTTGGTGATCAAGAGCGCGCAGATGAGGATGAGGTCACAGTACTTCTTCGGGTG 360	GTGACATATAATTTCATGAAGGATGGGTTCTTTCTAAAAGTAACA CCCAGACCCCAGGACCACACCAC		181 GGGGCTACACCTGCCGAGGAACAGGCTTGGCTCCCAGCAGCGGGGCCTGGACCTC 840	961 GTCTGTGCACACACACACCCCCCAGCCAGCTGAGCTGGACCCAGAGGGGACAGGTT 1020	1141   AGCTTCCGTGCACTACTCCCCGAAGCTGGTCCTTGCTCCTGGGAGGTTGAG   1200

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ya, E., Baker, K., Baldwin, D., Brush, J.,
Towley, C., Currell, B., Deuel, B.,
Grimaldi, C., Gu, Q., Hass, P.E.,
S., Kilmowski, L., Jin, Y., Johnson, S.,
Ark, M., Robbie, B., Sanchez, C.,
Simmons, L., Singh, J., Smith, V.,
Sim, Simons, C., Wieand, D., Woods, K.,
Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Johnski, P.,
Ery Initiative (SPDI), a Large-Scale
nan Secreted and Transmembrane Proteins: 1800 1620 CTCCCTCCCCAGAATCAAAGAAGAACCAGAAA 1740 CCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1620 p mRNA linear PRI 03-OCT-2003 GLEC10 (UNQ477) mRNA, complete cds. GCCTCCATGGAGGGCTCAGCTCCGGCCTCAGG 1380 SGGCCCAGAGTGGATCCATCCTGCAGCTGCCA 1440 CCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1860 Craniata, Vertebrata, Buteleostomi, Catarrhini, Hominidae, Homo. AGGCGGATTATGCAGAAGTCAAGTTCCAA 1917 AGGCGGATTATGCAGAAGTCAAGTTCCAA 1677 ment of Bioinformatics, Genentech, incisco, CA 94080, USA TCTCCCGGCACACACCACCAGATTACATC CTCCCTCCCCAGAATCAAAGAAGAACCAGAAA TCTCCAACGGAGCGTTTCTGGGAATCGGCATC TCTCCAACGAGCGTTTCTGGGAATCGGCATC TGATCATCATGAAGATTCTACCGAAGAGACGG TGATCATCATGAAGATTCTACCGAAGAGACGG CTCAGAAGCGGAATCAGAAAGCCACACCAAAC CTCAGAAGCGGAATCAGAAAGCCACACAAAC AACCCAAATCATCCACTCAAGCCCCAGAATCC TCTCCCGGCACACACGATCCTGGATTACATC (2003)

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Patent No. 659008
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TILE PERERENCE: 1488.048001
CURRENT APPLICATION: CD31-Like Protein
FILE REFERENCE: 1488.048001
CURRENT APPLICATION WUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR PILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3:1
SEQ ID NO 1
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Best Local Similarity 70.5
Matches 458; Conservative
FEATURE:
NAME/KESY: CDS
LOCATION: (37)..(1689)
OTHER INFORMATION:
NAME/KESY: sig_Deptide
LOCATION: (37)..(81)
OTHER INFORMATION:
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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946 GTAAGGTCTGCAGAAAAGGAGGCTTCACCTGCCGCGCTCAGCACCCGCTGGGCTTCCTG 1005
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APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/522,317
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
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Zhang, Jie
Ren, Feiyan
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Yang, Yonghong
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Liu, Chenghua
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Wang, Dunrui
Wang, Zhiwei
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38-09-620-312D-407
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361
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                                                                                                  122 GCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGT
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                                                      Gaps
                                                      4:
  Length 1488;
Score 177; DB 4; Length 14
Pred. No. 6.8e-35;
0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FO
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PC-OMPALIBLE
MEDIUM TYPE: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 TGCTCAGCTTCAGGCCC 438
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.
9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
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                                                   Matches 288; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 PORTER
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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1033 CTCTGCGCCTGGTCTGTCCTCTGAATCCCCCTGCCAGCTGAGCTGAGCTGGACCTGGG 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 171.4; DB 3; Length 70.5%; Pred. No. 1.8e-33; Live 0; Mismatches 96; Indels
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Sequence 1, Application US/09038832

Patent No. 6146845

GENERAL INFORMATION:
APPLICANT: KILLY, KRISTINE
APPLICANT: BRICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-2

TITLE OF SEQUENCES: (SAF-2)

NUMBER OF SEQUENCES: (SAF-2)

NUMBER OF SEQUENCES: (SAF-2)

ADDRESSEE: RAINER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE
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                                                                                                                                                            ATTORNEY PARTY.

REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-5018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 610-407-0701
TELEFAX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDENESS: single
TYPE: nucleic acid
STRANDENESS: single
                       FILING DATE: 11-MAR-1998
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 229; Conservative
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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STATE: PA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-038-832-3
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                    <u>ښ</u>
                                                                                                                                                                                                                                                                                                                      Length 1437;
                                                                                                                                                                                                                                                                                                                    Score 175.4; DB 4; Length Pred. No. 1.7e-34; O; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3. Application US/09038832
Fatent No. 6146845
Fatent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
TITLE OF INVENTON: Sialoadheain Family Member-2
TITLE OF INVENTON: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 1029:
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      9.1%;
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.2
Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                  ;
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CLONE: 9180097
US-09-023-655-1029
                                                                                                                                             STRANDEDNESS: sir
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          833 ATGCCACAGCATCCACAGCCCTGGGAAATGGCTCATCTCTTTCAGTCCTTGAGGGCCAGT 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09046736
[Pakent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Staloadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%; Score 171.4; DB 3
70.5%; Pred. No. 2.2e-33;
tive 0; Mismatches 96
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1130 ACGTCTCTCTCAGCCTCTCCGTGCA 1154
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                                                                                                                                                                                                                       GH-50018
                           MBER: US/09/038,832
11-MAR-1998
                                                                                           PRICR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-197
ATTORNEY/AGENT INFORMATION:
NAME: PREESTA, PAUL
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50017
TELECOMMUTICATION INFORMATION:
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                    TELEFAX: 0.00 TELEX: 846169
TELEX: 846169
TOPORMATION FOR SEQ ID NO: 1: 0.00 TELEX: 1.00 Dase pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %Query Match
Rest Local Similarity 70.5%
Matches 229; Conservative
                   CURRENT APPLICATION DA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                              CLASSIFICATION:
                                                           FILING DATE:
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TOPOLOGY:
MOLECULE TYI
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STAID.
COUNTY: USA
ZIF: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

STREET: P.O. Box 980 CITY: Valley Forge

CITY: STATE:

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1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1119 recretectricidarenentarianananasenetadeadaaaaaneeeadaadaa 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 TAGAGGGCGAGTCTCTGCGCTTGTTGTTTGACAGCAATCCCCCTGCCAGGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818 CCCAGCAGCGAGCCCTGGACCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 157.2; DB 3;
60.5%; Pred. No. 6.4e-30;
tive 0; Mismatches 188;
                                   SOPTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24 MAR.1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GH-50019
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                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,03:
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 60.59
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             FILING DATE: 24-MAK-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 610-407-07
TELEFAX: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-513-999C-522
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY APRORMATION:
NAME: PREStia, Paul F
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: 23,031
REFRENCE/DOCKET NUMBER: 33,031
TELESHONE: 610-407-0700
TELESHONE: 610-407-070
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; Sequence 11, Application US/08896537A
; Patent No. 6590088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%;
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1502 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.0°
Matches 282; Conservative
     COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-046-736-3
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Parent No. 6/183961
File REPERBNCE: 59.082.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Parent.pm
SEQ ID NO 5:22
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Parent No. 6090582

GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155.2; DB 4;
Pred. No. 1.1e-29;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               LOCATION: 62.109
OTHER INFORMATION: score 11.3
OTHER INFORMATION: seq PLLLSSLLGGSQA/MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 24
; OTHER INFORMATION: Xaa=Ala or Ser
US-09-513-999C-522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 179 TOTHER INFORMATION: k=g or t
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Best Local Similarity 98.2
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 85
OTHER INFORMATION: m=a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 178
OTHER INFORMATION: n=a,
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 62..229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
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1024 AGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCAC 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 TACCCCTCACAGCCCTCAAACCTCTGGTACTGGAGCTG---CAAGTGCACCTGGGGGAT 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 droacaracciccrcadaacrrdacrdroacrcrcrccaaddagaagcaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        904 GAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAAGCCTGTGCCTGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 ACAGCTCTGGGGAACAGCTCATCTTTCAGTCCTAGAGGGCCAGTCTCTGGCGTTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 TGTGTCACACACAGCAGCCCCCCAGCCAGCTGAGCTGACCCCAGAGGGGACAGGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 gaaggggaarrcaccrgrcaagcrcagaacrcrcaggarrcccagcacgrrrccrgaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    801 crcrccricchachachagrachachadchanantangacccrorntchaganaractaga
Score 152; DB 3; Length 15
Pred. No. 1.3e-28;
0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1262 GGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCG 1303
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APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
PILE REPRENCE: 1488.0480001
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
PRIOR PILING DATE: 1996-07-19
NUMBER: OF SEQ 1D NOS: 12
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (10)...(10)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
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HER INFORMATION: May be any nucleotide
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LOCATION: (340)..(341)
OTHER INFORMATION: May be any nucleotide
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OTHER INFORMATION: May be any nucleotide
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LOCATION: (415)..(416)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc_feature
LOCATION: (419)..(419)
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THER INFORMATION: May be any nucleotide
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HER INFORMATION: May be any nucleotide
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THER INFORMATION: May be any nucleotide
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         Gentz, Reiner L.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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LOCATION: (331)..(331)
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COCATION: (349)..(349)
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OCATION: (392)...(392)
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APPLICANT:
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RESULT 10

18-09-252-991A-5933/C

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18-09-252-991A-50-25-391A

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18-09-252-991A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-50-25-391A-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 CAAGGGGAACTGCTCGTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 CCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 eccadacadadadreaageceagadeceaggecegarreegecreerreggargreea 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GAAGAAGAACTGCTCCTGAGCATCGGAGATCCAGAANTGGAGGACACGGGAAGCTATTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 regecanagerrecegacegenagarecearacerrecerrenegriciesceacada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.1%; Score 78.4; DB 4; Length 459; 60.2%; Pred. No. 2.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                               OTHER INFORMATION: May be any nucleotide NAME/KEY: misc feature LOCATION: (434)...(434)
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (438). (439)
OTHER INFORMATION: May be any nuclectide
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LOCATION: (442). (443)
OTHER INFORMATION: May be any nucleotide
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OTHER INFORMATION: May be any nucleotide
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LOCATION: (449)..(450)
OTHER INFORMATION: May be any nucleotide
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; LOCATION: (459)...(459)
; OTHER INFORMATION: May be any nucleotide
US-08-896-537A-11
INFORMATION: May be any nucleotide
                                                                                                                                                                                                                                                                             INFORMATION: May be any nucleotide
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PRIOR FILING DATE: 1998-02-18
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity 60.24
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (436)..(436)
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LOCATION: (445)..(445)
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LENGTH: 1473
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2.9%; Score 54.8; DB 4; Length 1473; 50.0%; Pred. No. 0.00033;

Query Match Best Local Similarity

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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS.

FILE REFREBNCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 2295
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Pred. No. 0.00039;
0; Mismatches 137; Indels 0;
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ILING DATE: 2001-03-05
SEQ ID NOS: 948
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Patent No. 6783969
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US-09-252-991A-5939
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Zhang, Jie
Zhao, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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Best Local Similarity 50.0%;
Matches 137; Conservative
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
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Wang, Dunrui
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGENCES. 107196.136
CURRENT FILL OF DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190.
NUMBER OF SEG ID NOS: 33142
SEG ID NO 5956
                                                                        1325
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                                                                                                                               640 GGTGACCCTGTACGGCACCATGATCCTGAACTTCTGCGACTTCGCCCGCGCCTGCCCGGA
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Pred. No. 0.00036;
0; Mismatches 137; Indels 0
      Mismatches 137; Indels
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US-09-252-991A-5939
; Sequence 5939, Application US/09252991A
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5956
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Matches 137; Conservative
Matches 137; Conservative
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1415 AGAG 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             998 GCTGGACCCAGAGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGG 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1118 TGGGCTCCCAGCAGTCTCTCAGCCTCTCGGGCACTACTCCCCGAAG---CTGCTGG 1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763 GIGAAGGCIIGGGGAIITCAGGGCGCIIACACCIGCCGAGCGGAGAACAGGCIIIGGCICCCAG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 TAGAGGGGGAGACAGTCTCCATCTTGTTCCACACAGAGCAACCCGGACCCTATTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 ccarcrrcaaggagaagcagarccrgccacggccarcrrargagagrcagcrgcagcrgs
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CURRENT APPLICATION NATA:
APPLICATION NUMBER: 105/07/476,961
FILING DATE: 07-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 58,620
FILING DATE: 516,136
FILING DATE: 21-JUL-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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llarity 46.5%; Pred. No. 0.026;
Conservative 0; Mismatches 253; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 52; DB 4; Length 4059; Best Local Similarity 50.7%; Pred. No. 0.0024; Matches 152; Conservative 0; Mismatches 145; Indels
SOFTWARE: pt_PL_genes Version 2.0
                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                    NAME/KEY: CDS
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                   1295 ACTOCTTOGAGGTCACCCCCAGCTCAGCCGGGCCCTGGGCCCAACAGCTCCCTGAGCTCC 1354
                                                                                                                                                                                               1235 CGCCCCCTCTCTGCGCTGCTTGGGGAGGAGCTGCTGGAGGGGAACAGCAGCAGG 1294
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                                                                                                                                                                                                                                                            408 céchadochicerbechtrrendehecerreceschaesterbhadehedagada 467
288 ATGGCCAGAGAGCCACCGCCTTCAACCTGTCTGTGGAGTTTGCTCCCATAATCCTTCTGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    995 TGAGCTGGACCCAGAGGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1355 ATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCC
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                                                                                                                               317 gggrggrcgarcrggrccagccggrgcrcgacgggcrcgccccgggagaccggcgaacrgg
                                                                       468 GGGAGTITGIGIACTCAGAGGGGCAG---CGGCCTCCTGCTCACCAGCATCCTCACGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%; Score 45.2; DB 4; Length 861; 46.5%; Pred. No. 0.071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 46.5
Matches 186; Conservative
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Search completed: November 8, 2004, 20:38:24 Job time : 208.523 secs

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Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 117, Sequence 117, Sequence 117,

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US-09-999-832A-258

US-09-978-189-258

US-09-978-568A-258

US-09-978-564A-258

US-09-978-643A-258

US-09-99-833A-258

US-09-99-833A-258

US-09-99-833A-258

US-09-978-643A-258

US-09-978-643A-258

US-09-978-683A-258

US-09-978-258

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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1999-10-27
PRIOR PILING DATE: 1999-10-28
NUMBER: OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-052-586-117
US-10-174-590-117
US-10-176-758-117
US-10-175-737-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-984-130-15
, Sequence 15, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
                     Conservative
                     TYPE: DNA ORGANISM: Homo sapiens
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Best Local Simil
Matches 1911; C
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Sequence 15, Appl
Sequence 2, Appli
                                                                                                                              2004, 16:02:09; Search time 1338.51 Seconds (without alignments) 7711.054 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO6_MSO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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                         version 5.1.6
- 2004 Compugen Ltd.
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US-09-836-353A-15
US-09-910-600-2
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US-09-910-600-1
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                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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                                            Copyright
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Perfect score:
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DB 10; Length 2295;

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OY 1141 AGCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCTCCTGGGAGGCTGAG 1200	by 1201 GGTCTGCACTGCTCCTCCCAGGCCAGCCCGCCCTTTGGGGTGGCTT 1260  1258 GGTCTGCAGTGCTCCTCCCCAGGCCAGCCCGCCCCTTTTGGGGTGGTT 1317	Oy 1261 GGGGAGGAGCTGCTGGAGGGAACCAGCACCAGCACCTCCTTCGAGGTCACCCCCAGCTCA 1320	Oy 1321 GCCGGGCCCTGGGCCAACAGCTCCTGAGCCTCCATGGAGGCTCAGCTCCGGCCTCAGG 1380  Db 1378 GCCGGGCCCTACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGG 1437	Qy 1381 CTCCGCTGTGAGGCCTGGAACGTCCATGAGGCCCCAGAGTGGATCCATCC	1441 GATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1	1501 ACGGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCAAGATCTACCGAAGAGGGG 1	0y 1561 ACTCAGACCCGAGGCCCAGGTTCTCCCGGCACAGCATCCTGGATTACATC 1620  Db 1618 ACTCAGACAGACGCCGAGGCCCAGGTTCTCCCGGCACAGCACGGTCCTGGATTACATC 1677	1621 AANGTGGTCCCGAGGCTGGCCCCTGGCTCAAAGCGGAATCAGAAGCCACAAAC 1	1681 AGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGATCAAGAACAACCAGAAA 1740	AAGCAGTATCAGTTGCCAGATTCCCAAATCATCATCATCAGCCCAGAATCC 18	55—55 —55	Oy 1861 CTGAGGCCGGATGCCCAAGGCACCAGGCGGATTATGCAAGTTCAA 1917	RESULT 2 US-09-836-353A-15 ; Sequence 15, Application US/09836353A	GENERAL INFORMATION: ; APPLICANT: Ni et al. ; TITLE OF INVENTION: 12 Human Secreted Proteins	CURRENT APPLICATION NUMBER: US/09/836,353A ; CURRENT FILING DATE: 2001-04-18 ; FRIOR APPLICATION NUMBER: 60/198,407 ; PRIOR FILING DATE: 2000-04-19	PRIOR APPLICATION NUMBER: PCT/US99/25031 PRIOR FILING DATE: 1999-10-27 PRIOR PPLICATION NUMBER: 60/105,971 PRIOR PILING DATE: 1908-10-28	; NUMBER OF STATES OF STAT
61 TICTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120	1 IGCTCTTTCTCCTACCCCCACACACACACACACACACTCTACCCCAGCTTATGCTACTGC 1 IGCTCTTTCTCCTACCCCCACACACACACACACACACACAC	1 TICAAAGCAGTGACTGAACCAACCAAGGGGCCTCCTGTGGCCACAAACCACGAGTCGA TITCAAAGCAGTGACTGAGAACCAAGCGCTCCTGTGGCCACAAACCACCAGAGTCGA TITCAAAGCAACTAAACAAACAAACAAAACAAAAAAAAAA	1 GAGGTGGAAATGAGCACCCGGGGCCATTCCACTCACTGGGGATCCCGCCAAGGGAACCGGGAACCGGCAAGGGAACCGGCCAAGGGGAACCGGCCAAGGGGAACCGGCCAAGGGGAACCGGCCAAGGGGAACCGGCCAAGGGGAACCGGCCAAGGGAACCGGCCAAGGGAACCGGCCAAGGGAACCGCGGGGGCCGATTCCAGCTCCACCGGCAAGGGAACCGGCCAAGGGAAACAAGAACAACA	1 TGCTCCTTGGTGGTCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTCGGGTG	61 GAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTCTAAAAGTAACA 	421 GTGCTCAGCTTCACGCCCAGACCCCACAACACCGACCTCACCTCACCTGTGGAC 480	481 TICTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGGTGTGGCCTATGCCCCC 540	AGAGACCITGITATCAGCATTICACGIGACAACACGCCAGCCCTGGAGCCCCAGCCCCAG	601 GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 660	661 GACAGCCAGCCCCTGCCACACTGAGCTGCTGCAGAACAGAGTCCTCTCCTCGTCC 720 	CATCCTGGGGCCTAGACCCTGGGGCTGCTGCCGGGGTGAGGGTGGGGATTCA	781 GGGGGTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGGAGCCCTGGACCTC 840 	841 TCTGTGCAGTATCCTCCAAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 900	901 CTGGAAAACCTTGGGAACGGCACCTCTCCCAGTACTGGAGGCCAAAGCCTGTGCCTG 960 	961 GTCTGTGTCACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1020 	1021 CTGAGCCCTCCCAGCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080	1081 CACGAAGGAGTTCACCTGCCACGCTCGCACCCACTGGGCTCCCAGGACGTCTCTC 1140

	OY 1021 CTGAGCCCTCCCAGCCCTCAGAGCTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080	Oy 1081 CACGAAGGAGATTCACCTGCCACGCTCGGCACCCCAGGCACCCCCAGCACCTCTC 1140	1141 AGCTCTCCGTGCACTACTCCCCGAAGCTGTGGGCCCCTCCTGCTCCTGGGAGGCTGAG	GGTCTGCACTGCAGCTCCTCCCAGGCCGGGCCCCTCTCTGGGCTGGTTGTTTTTTTT	GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 	1321 GCGGGCCTGGGCCTCAAGACTCCCTGAGCTCCATGGAGGCTCAGGTCTCGGCCTCAGG 1378 GCGGGGCCTGGGCCAACAGCTCCTGAGGCTCCATGGAGGGTCAGGCTCAGG	1381 CTCGGTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC	1441 GATAAGAAGGGATCATCTCAACGGCATTCTCCAACGGACGTTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTGGGAATCGGCATTCTTCTTGGGAATCGGCATTCTTCTTGGGAATCGGCATTCTTCTTGTGGAATCGGCATTCTTCTTGTGGAATCGGCATTCTTCTTGTGGAATCGGCATTCTTCTTTTTTTT	Oy 1501 ACGGCTCTTCTTTCCTCGGCCTGGCCCTGATCATGAAAATTCTACCGAAAAGGGGG 1560	QY 1561 ACTCAGACAGAAACCCCGAGGTTCTCCCGGCACAGCACCAGCATCCTGGATTACATC 1620	CAGAAGCGGAATCAGAAAGCCACACCAAAC 	Oy 1681 AGTCTCGGACCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAGAAGAAGAAAA 1740	OY 1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCACGCCCAGAATCC 1800  DD 1798 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACACAGCCCCAGAATCC 1857	OY 1801 CAGAGAGCCAAGGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGAGG 1860	Oy 1861 CCTGAGGCCCGGATGCCCAAGGGCACTCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917	RESULT 3 US-09-910-600-2 ; Sequence 2, Application US/09910600	; PUBLICATION NO. USZUGJOSESIAL ; GENERAL INFORMATION: ; APPLICANT: Longphre, Malinda ; APPLICANT: Chang, Han ; APPLICANT: Whitney, Gena ; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
TYPE: DNA ORGANISM: Homo sapiens S-09-836-353A-15	99.5%; Score 1907.4; DB 10; Length 2295; arity 99.7%; Pred, No. 0; Airmarchot 6; Indel 0.	TGCTACTGCCACTGCTGCTGCTGCTGCGGGGGCCCAGGCTATGGATGG	1 TTCTGGATACGAGTGCAGGAGTCAGTGATGCCGGAGGGCCTGTGCATCTCTGTGCCCTGTGCATCTCTGTGCCCGAGGGCCTGTGCATCTCTGTGCCCGAGGCCTGTGACACTCTGTGCCCCCGAGGCCTGTGACATCTCTGTGCCCCC	121 TGCTCTTTCTCCTACCCCGACAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180	TTCAAAGCAGTGACTGAAGCAACCAAGGGTGCTCCTGTGGCCACAAACCACAGA	GAGGTGGAAATGAGCACCCGGGCCGATTCCAGCTCACGGGATCCCGCCAAGC	301 IGCTCCTIGGTGATCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360 	361 GAGAGGAAGCTATGTGAGATATATTCATGAACGATGGGTTCTTTCT	421 GTGCTCAGCTTCACGCCCAGACCCCAGGACCACCACCTCACCTGCCATGTGGAC 480	TTCTCCAGAAAGGGTGTGAGGCGACAGAGGACGGTCCGACTCCGAGTGTGGCCTATGCCCCC	AGAGACCTIGITATCACCATTTCACGTGACAACGCCGGCCCGGGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCCAGGCCCCCAGGCCCCCC	GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGCGCTCCTCTGTGCTGCTCTGCTGCTGCTGCT	GACAGCCACCTGCCACACACACAGGGTCCTGCAGAACAGAGTCCTCCCTC	CATCCTGGGGCCCTAGACCCTGGGGCTGGAGTGCCGGGGTGAAGGTGGGGGTGAAGGTGGGGGTTGAAGGTGGGGGG	GGGGGTACACCTGCCGAGCGGAGAAAAGGCTTGGCTCCCGGGGGGGAGGAGGCTGGGGGCTCCGGGGGGGG	841 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGAAGGTC 900 	901 CTGGAAAACCTTGGGAACGACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 960 

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RESULT 4
US-09-910-600-15
Sequence 15, Application US/09910600
PUDICATION NO. US20030036631A1
GENERAL INFORMATION:
APPLICANT: LONGPARE, Malinda
APPLICANT: Congphre, Malinda
APPLICANT: Congphre, Malinda
APPLICANT: Mitney, Gena
TITLE REFERENCE: DO003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT PILING DATE: 2000-07-21
FRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.03
BRIOR PILING DATE: 2000-07-21
MUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.03
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Pred. No. 0;
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Best Local Similarity 91.7%;
Matches 1917; Conservative
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US-09-910-600-15
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US-10-614-683-9

j Sequence 9, Application US/10614853

j Publication No. US20040138114A1

j GENERAL INFORMATION:
   APPLICANT: HILARY CLARK
   APPLICANT: HILARY CLARK

APPLICANT: HILARY CLARK

APPLICANT: HILLIAM FONG

APPLICANT: HILLIAM WOOD

APPLICANT: HILLIAM WOOD

APPLICANT: HILARY CONSTITIONS AND METHODS FOR THE TREATMENT OF INMUNE

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF INMUNE

TILLE OF INVENTION: RELATED DISEASES

TILLE OF INVENTION NUMBER: US/10/614,853

CURRENT PILING DATE: 2003-07-08

PRIOR FILING DATE: 2002-07-08

NUMBER OF SEQ ID NOS: 28

SEQ ID NOS: 28
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                                          CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGGCTCCGGCCTCAGGCTCCGC
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90.2%; Score 1729.8;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1915; Conservative 0; Mismatches
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CORGANISM: Homo sapien
US-10-614-853-9
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OTHER INFORMATION:
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LOCATION: (26)
OTHER INFORMATION:
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                                                                                    GTCACACACAGCAGCCCCCCAGCCAGCCTGAGCTGGAACCAGAGGGACAAGGTTCTGAGC
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    AACCTTGGGAACGGCACGTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT
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Publication No. US20030055231A1

355017 7 35-09-984-130-148

GENERAL INFORMATION:
APPLICANT: Ni et al,
TITLE OF INVENTION: 12 Human Secreted Proteins FILE REPERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/24,792
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR PILING DATE: 2001-04-18
PRIOR PLING DATE: 2000-04-19
PRIOR PLING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 67/1089/25031
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR APPLICATION NUMBER: 66/105,971
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 149 υ υ υ O υ υ O FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE LOCATION: (11) LOCATION: (31)
OTHER INFORMATION: n equals a,t,g, or NAMES/KEY: SITE
LOCATION: (32) Ö ö ör Ö ö or ö ö NAME/KEY: SITE LOCATION: (6) OTHER INFORMATION: n equals a,t,g, OTHER INFORMATION: n equals a,t,g, NAME/KBY: SITE LOCATION: (25) OTHER INFORMATION: n equals a,t,g, LOCATION: (29) OTHER INFORMATION: n equals a,t,g, NAME/KEY: SITE INFORMATION: n equals a, t, g, INFORMATION: n equals a,t,g, INFORMATION: n equals a,t,g, n equals a,t,g, a,t,g, n equals n equals n equals Patentin Ver. 2.0 ORGANISM: Homo sapiens OTHER INFORMATION: NAME/KEY: SITE

GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTTGTGCTGCTGACGCCCAGCCCAGCCCACCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCCTGCAGCCCCTGCAGCCCCTGCCTG			
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OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (33) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (34) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (37) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (38) OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (38) OTHER INFORMATION: n equals a,t,g, or c -09-984-130-148 Ouery Match Bast Local Similarity 91.6%; Score 1729.8; DB 10; Length 2338; Bast Local Similarity 91.6%; Pred. No. O; Mismatches 2; Indels 174; Gaps 1	CCACTGCTGCTGCTCGCTGGCGGGGTCCCAGGCTATGGATGG	241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCGGGGATCCCGCCAAGGGGAAC 300 441 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 500 401 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGAAC 500 301 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGAGACACACAC	621 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCGGGCGGG
Mae - 0			

	1339   TOAGCCTCTCCGTGCACTACTCCCCGAGCCCTCTCTGCGCGCCTCTGCGCGCGC	1439 1258 1318 1559 1378 1619	0y         1679 AGACTCCTCGGACCCTCTTCCACGGGGGCCCCCGGGATCAAGAAGAACGAA         1738 AAAGCACTCTTCCACGGGGCCCCCCCCGGAATCAAGAAGAACAACAAGA         1557           0y         1739 AAAAGCACTATCAGTTGCCCAGTTTCCCAGAATCCACCACACCCCAGA         1557           0y         1739 AAAAGCAGTATCAGTTGCCCAGTTTCCCAGAATCATCCACTCAAGCCCCAGAAT         1798           0y         1799 CCCAGGAAGCCAAGAGGTTTCCCAGAACCCAAATCATCCAGCCCCAGAAT         1617           0y         1799 CCCAGGAAGCCAAGAGGTTTCCCAGAACCCAAATCATCCCAGCCCCAGAAT         1617           0y         1799 CCCAGGAAGCCCAAGAGGTTCCCATTATGCCACGCTCAACTTCCCAGGCCTCAGACCCA         1677           0y         1859 GCCTGAAGAGCCCCAAGAGGCCCCAAGAGCCCCAAGAGCTCAACTTCCCAGGCGTCAGACCCA         1677           0y         1859 GCCTGAAGAGCCCCAAGAGGCACCCAAGGCGCTCAACTTCCCAGGCGTCAGACCCA         1677           0y         1859 GCCTGAAGACCCCAAGAGGCACCCAAGGCGCTCAACTTCCCAGGCGTCAGACCCCA         1677           0y         1878 GGCTGAAGGCCCCAAGAGGCACCCAAGGCGCACAAGGCACCAAGAGTCCAAATTTTCCAAGATCCAA         1677           0y         1878 GGCTGAAGGCCCCAAGAGGCACCCAAGGCCCCAAGAGTCCAACAAGTCCAA         1677           0y         1878 GGCTGAAGGCCCCAAGAGGCCCCAAGAGGCCCCAAGAGTCCAACAATTATGCAAAGTTCCAA         1677           0y         1878 GGCTGAAGGCCCCAAGAGGCCCCAAGAGGCCCCAAGAGTCCAAAATTATGCAAAATTCCAAAATTCCAA         1677	<pre>costs of the control of the con</pre>
1747 TATCACTTGCCCAGATTCCCAGAATCATCCACTCAAGCCCCAGAATCCCAGGAG 1806	REGULT 8  GGUERGE 3, Application US/09910600  Publication No. US20030036631A1  GGENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Change, Malinda APPLICANT: Change, Han APPLICANT: Change, Han APPLICANT: Mitteey, Gena APPLICANT: Mitteey, Gena APPLICANT: Mitteey, Gena APPLICANT: Mitteey, Gena TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF FILE REFRERENCE: D0003NP FILE REFRERENCE: D0003NP FILING DATE: 2001-07-20 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 32 SECTIVARE: Patentin Ver. 2.0 SEQ ID NOS: 32 LENGTH: 2823 LENGTH: 2823 LENGTH: 2823 LENGTH: CRANISM: Homo sapiens	Best Local Similarity   99.9%;   Pred. No. 0;   Matches 1498;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;   Matches 1498;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;   0;   0;   0;   0;   0;   0;   0	Oy   659 AGGAAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTGCGGGCTCCTCTGCTG   658	58 icterdigeadatecrecadadadecrecadagaderineceadecadagada 717 b Oy 899 recregaaaaceteggaacggcacgtereceagaaacggcaaagcgtgtge 958

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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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FILING DATE: 1998-03-27
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PPLICATION NUMBER: 60/079923
TLING DATE: 1998-03-30
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ING DATE: 1998-03-31
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ILING DATE: 1998-03-31
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LING DATE: 1998-04-01
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LING DATE: 1998-04-08
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APPLICATION NUMBER: 60/080327
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PLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/083392
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1704 CCTGAGGCCCGGATGCCCAAGGGCACCCAGGGGATTATGCAGAAGTCAAGTTCCAA 1760
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                                                                                                            Sequence 258, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Christopher
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING TION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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FILING DATE: 1997-10-17
FILING DATE: 1997-11-03
FILING DATE: 1997-11-13
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SICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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PLICATION NUMBER: 60/078939
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PLICATION NUMBER: 60/079294
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Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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Paoni, Nicholas F.
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Desnoyers, Luc
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Grimaldi, J. C
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Baker Kevin P.
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Tumas, Daniel
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IOR FILING DATE: 1998-04-29 IOR APPLICATION NUMBER: 60/083495	& £	121 TGCTCTTTCCTACCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTAGT 180
APPLICATION NUMBER: 60/08349 FILING DATE: 1998-04-29	8 8	[
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IOR APPLICATION NUMBER: 60/083545 IOR FILING DATE: 1998-04-29 IOR APPLICATION NUMBER: 60/083554 IOR FILING DATE: 1998-04-29	& A	241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 300 [
IOR APPLICATION NUMBER: 60/083558  IOR FILING DATE: 1998-04-29  IOR APPLICATION NUMBER: 60/083559	8 8	301 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCAGGTACTTCTTTCGGGTG 360 
IOR FILING DATE: 1999-04-29  IOR PILING DATE: 1998-04-29  IOR PELLING DATE: 1998-44-30	yo da	
IOR APPLICATION NUMBER: 60/084366 IOR FILING DATE: 1998-05-05 IOR APPLICATION NUMBER: 60/084414 IOR APPLICATION NUMBER: 60/084414	λ o o	421 GTGCTCAGCTTCACGCCCAGACCCCAGACACACAGACCTCACCTGCCATGTGGAC 480
IOR APPLICATION NUMBER: 60/084441  IOR FILING DATE: 1998-05-06  IOR APPLICATION NUMBER: 60/084637  IOR PILING DATE: 1998-05-07	Qy	481 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGCCCTATGCCCCC 540
IOR APPLICATION NUMBER: 60/084639  IOR FILING DATE: 1998-05-07  IOR PILING DATE: 1998-05-07  IOR FILING DATE: 1998-05-07	QQ qq	541 AGAGACCTIGITATCAGCATITCACGAGACACACGCCAGCCCTGGAGCCCCAGGCCCCAG 600
IOR APPLICATION NUMBER: 60/084598  IOR FILING DATE: 1998-05-07  IOR APPLICATION NUMBER: 60/084600  IOR APPLICATION NUMBER: 60/084600	QY DP	601 GGAAATGTCCCATACCTGGAAGCCCAAAAAGCCCAGTTCCTGGGGCTCCTCTGTGCTGCT 660
IOR APPLICATION NUMBER: 60/084627 IIOR FILING DATE: 1998-05-07 IIOR PILING DATE: 1998-05-07	Qy	661 GACAGCCCCTGCCACTGAGTGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC 720
IOR APPLICATION NUMBER: 60/085339 IOR FILING DATE: 1998-05-13 IOR PILING DATE: 1998-05-13 IOR PILING DATE: 1998-05-13	& 8	721 CATCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCGGGGTGAAGGCTGGGGATTCA 780
IOR APPLICATION NUMBER: 60/085323  IOR FILING DATE: 1998-05-13  IOR PIPLICATION NUMBER: 60/085582  IOR PIPLICATION DATE: 1998-05-15	상 업	781 GGGGGTACACCTGCCGAGGGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCTTGGACCTC 840
IOR APPLICATION NUMBER: 60/085700 IOR FILING DATE: 1998-05-15 IOR APPLICATION NUMBER: 60/085689 IIOR PILING DATE: 1998-05-15	% व	841 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 900
IOR APPLICATION NUMBER: 60/085579 IOR FILING DATE: 1998-05-15 IOR APPLICATION NUMBER: 60/085580 IOR PILING DATE: 1998-05-15	දු පු	901 CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 960 
IOR APPLICATION NUMBER: 60/085573 IIOR FILING DATE: 1998-05-15 IIOR APPLICATION NUMBER: 60/085704 IIOR FILING DATE: 1998-05-15	oy da	961 GTCTGTGTCACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCAGAGGGACAGGTT 1020 1006 GTCTGTGTCACACAGCAGCCCCCCAGCCGAGCTGAGCTG
APPLICATION NUMBER: 60/085697 Match ocal Similarity 85.0%; Pred. No. 0;	상 염	1021 CTGAGCCCTCCCAGCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080 1066 CTGAGCCCTCCCAGCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1125
hes 1630; Conservative 0; Mismatches 2; Indels 285; Gaps  1 ATGCTACTGCTGCTGCTCCTCGCTGCTGCTGCTCCCAGGCTATGGATGG	% q	1081 CACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACGGGCTCCCAGCACGTCTCTCT 1140
ATGCTACTGCCACTGCTGCTGCTCGCTGCTGGGGGGGTCCCAGGCTATGGATGG	& 93	1141 AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGCCCCTCCTGCTCCTGGGAGGCTGAG 1200 [
TCTCT	λō	1201 GGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCGTGGTGGCTT 1260

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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
                                                                                         Tumas, Daniel
Williams, P. Mickey
Wood, William I.
      Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                   APPLICANT:
APPLICANT:
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equence 258, Application US/09978697 Scent No. US20020169284A1 ENERAL INFORMATION: rimaldi, J. Christopher errara, Napoleon ilvaroff, Ellen ong, Sherman Gerber, Hanspeter Gerritsen, Mary E urney, Austin L Botstein, David Soddard, Audrey Desnoyers, Luc Eaton, Dan Wei-Qiang ., Paul Baker Kevin P. GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi Ferrara, Godowski ong, 09-978-697-258 APPLICANT: PPLICANT PPLICANT LICANT PPLICANT PPLICANT Sequence

illan, Kenneth

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Napier, Mary A Pan, James;

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ON NUMBER: 60/080327

LING DATE:

1998-04-03

APPLICATION NUMBER: 60/080333

LING DATE: 1998-04-01

FILE OF INVENTION: ACIGGS ENCOCHING THE SAMES
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILMG DATE: 2001-10-16
PRIOR PELING DATE: 2001-07-30
PRIOR PELING DATE: 2001-07-30
PRIOR PELING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PELING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06311
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PRIOR APPLICATION NUMBER: 60/06311
PRIOR APPLICATION NUMBER: 60/07450
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PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07764
PRIOR PELING DATE: 1998-03-11
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PRIOR PELING DATE: 1998-03-20
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REILING DATE: 1998-04-08

REILING DATE: 1998-04-09

REILING DATE: 1998-04-15

REILING DATE: 1998-04-22

REPLICATION NUMBER: 60/081392

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REPLICATION NUMBER: 60/081392

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PRIOR PILING DATE: 1998-03-13
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PRIOR APPLICATION NUMBER: 60/079664
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PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-23
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PRIOR PRICATION NUMBER: 60/083495
PRIOR PRILING DATE: 1998-04-29
PRIOR PRILING DATE: 1998-04-18
PRIOR PRINCATION NUMBER: 60/08559
PRIOR PRINCATION NUMBER: 60/08559
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Eaton, Dan
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                                                            Objecty Match 69.6%; Score 1333.8; Ped. Local Similarity 85.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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	Sequence 258, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P. APPLICANT: Betsein, David	Sequence 25 Publication GENERAL INF APPLICANT: APPLICANT:	3
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APPLICATION NUMBER: 60/083559
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FORT. PROPERTY REALY.

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ICONT. Peori, Manchase F.

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ILCONT. Persart, Timerby A.

ILCONT. Persart,
                                                                               Godowski, Paul J.
Godowski, Paul J.
Gurimaldi, J. Christopher
Gurney, Austin J.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napler, Mary A.
                  Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
        Sherman
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346 TGCTCCTTGGTGATCAGACGCGCAGATGCAGGATGACTACTTTCGGGTG		1006	1021 CTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCTGGAGTTCAAGTGGAG   1080   1066   CTGAGCCCTCCGGGTTCAAGTGGAG   1080   1066   CTGAGCCCTCCCAGCCTCCAGCCTCGGGTTCAAGTGGAG   1125   1081   CACGAGGCCTCCAGCCTCGGGTTCAGTGGAG   1125   1126   CACGAAGGAGTTCACCTGCCAGCACCCACTGGGGTTCCTCTC   1140   1111	GCGGGCCCTGGGGGAACGCCTGGGCCAGGCCGGCCCTTCGAGGTCACCCCCAGCTCA GCCGGGCCCTGGGGGAACAGCTCCTTGAGGCTCCTTCGAGGTCACCCCCAGCTCA GCCGGGCCCTGGGCCACAGGCTCCCTGAGCCTCCTTGGAGGCTCAGGCTCAGG
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PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083500 PRIOR APPLICATION NUMBER: 60/083742 PRIOR PLING DATE: 1998-04-30 PRIOR PILING DATE: 1998-04-30 PRIOR PILING DATE: 1998-04-30 PRIOR PILING DATE: 1998-05-05 PRIOR PILING DATE: 1998-05-06 PRIOR PILING DATE: 1998-05-07	APPLICATION PARTS FILLING DATE: APPLICATION PILLING DATE: APPLICATION	APPLICATION NUMBER: PILING DATE: 1998-05 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-05	## PRIOR APPLICATION NUMBER: 60/085697  Query Match  Bast Local Similarity 85.0%; Pred. No. 0;  Bast Local Similarity 85.0%; Pred. No. 0;  Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;  A Matches 1630; Conservative 0; Mismatches 2; Mismat	121 TGCTCTTTCCCCCGACAGGCTCTACCCCCGGCTTATGGCTACTGG 180  166 TGCTCTTTCTCCTACCCCGACAGGCTCTACCCCCGGCTTATGGCTACTGG 225  161 TTCAAAGCAGTGACTCAAGGCTGCTCCTGTGGCCACAAACCACAGGTTATGGCTACTGG 225  181 TTCAAAGCAGTGACTGAGACAACGAAGGGTCCCTGTGGCCACAAACCACAGGTCGA 240  182 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGGTCGA 285  241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 300  286 GAGGTGGAAATGAGCCCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 345  301 TGCTCCTTGGTGATCAAGACCCGCGCCGATTCCAGCTCACTGGGGATCCTGCTCGCGGAAC 345  101 TGCTCCTTGGTGATCAAGACCCGCGCATTCCAGCTCACTGGGGATCCTGCTCGCTGTGGTGATCTTTCGGGTG 360

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                                 1202 -ATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1260
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1441 GATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1500
                                                                                                                                    1261 ACGCTCTTCTTTTCTCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG 1320
                                                                                                                                                                                                         1561 ACTCAGACAGAAACCCCGAGGCCCCAGGTTCTCCCGGCCACAGCACGATCCTGGATTACATC 1620
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
                                                                                                         1501 ACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATGAAGATTCTACCGAAGAGAGGG
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Filvaroff, Ellen
Fong, Sherman
Gao, Wal-Qiang
Gerber, Hanspeter
Gerderd, Audrey
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: ABARCHAZI, AVI
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Kuo, Sophia S.
Napier, Mary A.
Pan, James,
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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R APPLICATION NUMBER: 60/079656

R APPLICATION NUMBER: 60/079664

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R APPLICATION NUMBER: 60/080333
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R APPLICATION NUMBER: 60/081070
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R APPLICATION NUMBER: 60/066364

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APPLICATION NUMBER: 60/081071
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	2764;	atggatgggaga              atggatgggaga	CTCTG 	ATGGCT        ATGGCT	DACCAGAGTCGP                 DACCAGAGTCGA	0GCCAAGGGGAAC	GAGGIGGAAARISAAGCACCCCGGGGCCGGGTTCCCGCGCTCGCGGGGATCCCCGCGCGAAGGGGGGTTGCTGCGGGTTGCTCTTTCGGGTTTCTTTC	CTTTC	TGGGTTCTTTCTAAAAGTAACA 	CCATG	CTATG		CTGTG		CTCCT	GAAGGCTGGGGATTCA	TGGG
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	e 133. No.	CTCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTTCTTCTT	GTGAT       GTGAT	CCGACAGGACTGGAC 	AAGGG       AAGGG	CGATT	CAGAT	CAGAT	AATTT       AATTT	CAGGA        CAGGA	CAGAG	CACGTGACAAC	CAAAA	SCCCAAAAAGGCC	TGAGCTG         TGAGCTG	9	.T.0999
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Oy 781 GGGGGTACACCTGCCGAGGGAAACAGGCTTGGCTCCCAGCAGCGAGCCTGGACCTC 840 	Qy         841         TCTGTGCAGTATCCTCCAGAGAACCTGAGGATGATGGTTTCCCAAGGAAACAGGACAGTC 900           Db         886         TCTGTGCAGTATCCTCCAGAGAACCTGAGGTGATGGTTTCCCAAGCAAACAGGACAGTC 945           Qy         901         CTGGAAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGCCAAAGCCTGTGCCTG 960	ACAGGTT 1	1021		QY         1141 AGCCTCTCGGTGCACTACTCCCGGAAGCTGCTGCTCCTGCTCCTGGGAGGCTGAG 1200           Db         1186 AGCCTCTCCGTGCACTC1201	QY 1201 GGTCTGCACTGCAGCTGCTCCCAGGCCAGCCCGGCCCCTCTCTGCGCTGGTGGCTT 1260	Db	1202	QY 1321 GCCGGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGGCTCCGGCCTCAGG 1380	Db 1202 1201 Oy 1381 CTCGGCTGTGAGGCTGGAACGTCCAGGGGCCCAGAGTGGATCCATCC	1202	QY       1441 GATAAGAAAGGGACTCATCTCAACGGAGCGTTTCTGGGAATCGGAATC       1500         DD       1202 -ATAAGAAGGGATCATCTCAACGATTCTCCAACGAGCGTTTCTGGGAATCGGCATC       1260	QY 1501 ACGGCTCTTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGAGG 1560  Db 1261 ACGGCTCTTCTTTCCTCTGCTGGCCTGATCATCATGAAGATTCTACCGAAGACGG 1320	OY 1561 ACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGACCGATCCTGGATTACATC 1620	OY 1621 AATGTGGTCCCGACGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAAC 1680 	QY 1681 AGTCCTCGACCCTCTTCCACCAGGTGCTCCCTCCCCCAGAATCAAGAACCAGAAA 1740  Db 1441 AGTCCTCGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAACCAGAAA 1500	OY 1741 AAGCAGTATCACTGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1800 	Oy 1801 CAGGAGAGCCAAGAGCACCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCAGG 1860

		Qy 1381 CTCCGCTGTGAGGCCTGGA
<b>18</b> 1-2	TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG	1202
بر چين و	346 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 405 361 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	
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	GGAAATGTCCCATACCTGGAGCCCAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT	1681
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i≱ g	841 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAG	Search completed: November 9, 20 Job time : 1363.51 secs
. A. Q	901 CTGGAAAACCTTGGGAAGGGCAGGTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 960 	
A .0	961 GTCTGTGTCACACACAGCACCCCCAGCCAGCTGAGCTGGACCCGAGAGGGGAACGGT 1020 	
<b>2</b> 0	1021 CTGAGCCCTCCCGGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCCGGTTCAAGTGGAG 1080	
`. <u>&amp;</u>	1081   CACGAAGGAGTTCACCTGCCACGCTCGGCACCCACGGCTCCCAGCACGTCTCTCT   1140	
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<b>*</b>	1201 GGTCTGCACTGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTGCGCTGGTGGCTT 1260	
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881 CTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCTGCAGCTGCCA 1440	202 1201	G.	202 -ATAAGAAGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1260	501 ACGGCTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGGC 1560	261 ACGGCTCTTCTTCTCTCTGCTGGCCCTGATCATCATGAGATTCTACCGAGGAGGCG 1320	561 ACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATC 1620	321 ACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCAGCATCCTGGATTACATC 1380	521 AATGTGGTCCCGACGGCTGGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACAAAC 1680	181 ANTGIGGICCCGACGGCIGGCCCCTGGCICAGAAGCGGAAICAGAAAGCCACACCAAAC 1440	881 AGECCEGGACCCECTECTECACCAGGIGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA 1740	441 AGICCICGGACCCCICCTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA 1500	741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACGCCCAAGAATCC 1800	501 AAGCAGTATCAGTTGCCCAGATTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1560	801 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCACACCCAGG 1860	561 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1620	361 CCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917	szi ectgaggeceggargeceaagggecaecaggeggartatgeaaaggeaagtrecaa 1677
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Homo sapi PRODG1GID

tigr-gss-BS3000010

EM104791 506045 MA CF366716 841409 MA CE060061 tigr-gss-

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876 bp mRNA linear EST 16-JUL-2002
_7977108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215765
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30336415.
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910 bp mRNA linear EST 07-APR-2004
8324896 Homo sapiens PlACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI071YN14 5-PRIME, mRNA sequence.
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sapiens (human)

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BX324896.2 EST.

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SSPEGWLNRSPLYGYWFKGIRKPGLSFPVATUNKDKVLZBEARGRFCLGGISKKNC
SLLI KDVQMODSTNYFFRRAGFRFSFREFRLQVBALTQVBALTQVBDIFTFEUGDISKKNC
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GRAGHGAGTAGTTSVLLAPROSAFFSKGAVLGFGITALLALLALLEGEL
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/dev_stage="3 days neonate"
                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; putative weakly similar to SIALIC ACID-BINDING LECTIN [Homo sapiens] (SPIR]096RL6, evidence: FASTY, 61.6%ID, 84.6%length, match]19)"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
  Nature 409, 685-690 (2001)
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Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SIALIC ACLO-BINDING LECTIN [Homo sapiens], full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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       1049 GGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGAAGGAGAGAGTTCACCTGCCACGCTC
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High-efficiency full-length cDNA cloning
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HTC; CAP trapper.
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st Local Similarity 75.4%; Pred. No. 2.7e-168; éches 937; Conservative 0; Mismatches 288; Indels 18; Gaps 3; 419 cagnormanormentaloricana (1988)	6 CAGTTCTGAGCTTTATCCCAGGACTTCAACACCATGATACTGAGCTCACATGG	479 ACTICTCCAGAAAGGGTGTGAGGGCACAGAGGACCGTCCGACTCGTGGCCTATGCCC 538	539 CCAGAGACCTIGTIATCAGCATTICACGIGACAACACGCCAGCCCTGGAGCCCCAGCCC 598	599 AGGGAAATCTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTG 658	659 CTGACAGCCCCCTGCCACACTGAGCTGCTCTGCAGAACAGAGTCCTCTCCTCGT 718	719 CCCATCCTGGGGCCCTAGACCCCTGGGGCTGCAGCTGCCGGGGTGAAGGCTGGGGATT 778	779 CAGGGGGTACACCTGCCGAGGGGAGAACAGGCTTGGCTCCCAGCAGCGGGGCCTGGACC 838	839 TCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAG 898 1144 TCTCTGTGCTGTACCCCCCACAGGACCTGAGAGTGACTGTTTCCCAAGGAAACAGGACG 1203	899 TCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGGCCAAAGCCTGTGCC 958 1204 TGTTGGAAATCCTCAGGAATGCCATCTCCCTCGCAGTCCTGGAGGCCAAAGCCTGTGCC 1263	959 IGGICTGIGICACACACACAGCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGG 1018	1019 TTCTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGG 1078	1079 AGCACGAAGGAGAGTTCACCTGCCACGCACCCACTGGGCTCCCAGCACGTCTCTC 1138		1199 AGGGTCTGCACTGCACCTCCTCCCAGGCCAGCCCGCCCTCTCTGCGCTGGTGGT 1258	1259   TTGGGGAGGAGCTGCTGGAGGGAACAGCAGGACTCCTTCGAGGTCACCCCCAGCT   1318	1319   CAGCGGGCCCTGGGCCAACACCTCCTGAGCCTCCATGGAGGCTCAGCTCCGGCCTCA	1379   GGCTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCCAGAGTGGATCCATCC	1439 CAGATAAGAAGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGCA 1498

1744 CTGATAAAGACAGTGCCACAGCATTCTCCAAGGAGCAGTTTTGGGCTTTGGCA 1797 1499 TCACGGCTCTCTTTTCCTCTGCCTGGCCCTGATCATCAAGAAGATTCTACCGAAGAAGC 1558 1798 TCACGGCTCTTGCCTGCCTGGCCTGATCGTGAAGATTCTACCGAAGAAAG 1857 1559 GCACTCAGAACCCCTGCCTGCTCTCCCGGCAGCAGAAGAAAG 1857 1559 GCACTCAGAACCCCGAGGCCCAAGCTCTCCCGGGCAGCAGCACCTGGATTACA 1618 1858 GAACCCAGGAGAACCCTCAGGCCCAAGCTCTCCCGGGGCACCAGATCCTGGATTACA 1917 1619 TCAATGTGGTCCCGACGGCTCGCCTCGGCTCAGAAGCGAA 1661 1619 TCAATGTGGTCCCGACGGCTCCCTGGCTCAGAAGCGAA 1661 1918 TCAATGTGGTCCCCAAGACCCTCGGCTCCGAATTGGAA 1960	AK036698  AK036698  AK036698  MARA linear HTC 03-APR-2004  MARA musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830164423 product:weakly similar to SIALIC  ACID-BINDING LECTIN [Homo sapiens], full insert sequence.  AK036698.1 G1:26331615  HTC; CAP trapper.  MAR musculus (house mouse)  SM Mus musculus (house mouse)  Mas musculus (soureand to the sequence)  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  E 1  Carninci, P. and Hayashizaki, Y.  High-efficiency full-length cDNA cloning  L Meth. Enzymol. 303, 19-44 (1999)  10349636			FARTON CONSORTIUM. FARTON CONSORTIUM. FARTON CONSORTIUM and the RIKEN Genome Exploration Research S The FANTOM CONSORTIUM and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs  E 66,770 full-length CDNAs  E 783-573 (2002)  E 6 (bases 1 to 3939) S Adachi,U, Aizawa,K. Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hiraoka,T., Hayashida,K., Ishii,Y., Itoh,M., Kagawa,T., Kaukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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/db_xref="d1:26331616"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                       Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://fancom.gsc.riken.jp/
URL:http://fancom.gsc.riken.jp/
Location/Qualifiers
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Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Sakai,Y., Sakai,Y., Sakazume,N., Sano,H., Y., Saski,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGAGTOCTOTOCTOGTOCCATOCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCG
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Pred. No. 4.6e-148;
0; Mismatches 342;
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/mol_type="mRNA"
/strain="C5TBL/6J"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                          BF663289 936 bp mRNA linear EST 21-DEC-2000 60214414F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297851 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1014 ACAGGTTCTGAGCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCA 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 GTGCCTGGTCTGTGTCACACACACAGCAGCCCCCAGGCTAGGCTGGACCTGGACCCAGAGGGG 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov
Plate: LiCMN152 row: k column: 04
High quality sequence stop: 661.
Location/Oualifiers
rce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 936)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                              1888 CAGGCGGATTATGCAGAAGTCAAGTTCCA 1916
                                                                                                                                                        3636 TATTCTGATTACACAGAGGTCAGAGTCCA 3664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                   BF663289.1 GI:11937171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BF663289
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Best Local Similarity
Matches 705; Conserv
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KEYWORDS
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TITLE
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F663289
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1492
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EX283650 NIH MGC 48 Homo sapiens cDNA clone IMAGP958K041152 ;
IMAGE:429785I, mRNA sequence.
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
I bases 1 to 503.
Ebert, L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Umpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free from RZPD; contact RZPD (clonearzpd.de) for further information. Seq primer: pCMV-M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT. Location/Qualifiers
                                                                                                                      CTCTCTCAGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCCTCCTGCTCCTGGGA
                                                                                                                                                                                                                                     CTCTCTCAGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTGGGA
                                                                                                                                                                                                                                                                                                                                1194 GGCTGAGGGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTG
                                                                                                                                                                                                                                                                                                                                                               420 GTGGCTTGGGGAGGAGCTGCTGGAGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCC
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RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
bin/ShowLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Gromforschung GmbH Fax: +49 30 32639 101
Fax: +49 30 32639 111
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/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670 ccgacaagacrggacagggrcracccagcrrarggcracrggrrcaaagcagrgacrga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 CAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGT-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 GAGATATAATTTCATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCC
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                                                              networks
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling network:
Control human ES cell growth and differentiation
L Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650,473 7668
Fax: 650,473 7766
Email: rbrandenberger@geron.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryonic
                                                                                                                                                                                                                                                                                            Email: rbrandenberger@geron.com
Insert Length: 730 Std Error:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="GRN ES"
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Best Local S:
Matches 608
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                                                                                                               JOURNAL
COMMENT
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(bases 1 to 730).
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
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17000424511003 GRN ES Homo sapiens cDNA 5', mRNA sequence.
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                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity 100.
Matches 505; Conservative
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736 AGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGCTACACCTGC 795
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                                     108 AGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTCAGGGCGCTACACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905 Homo sapiens sialic
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/2001
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Holzman,T.
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                                                                            796 CGAGCGCAGACACAGCTTGCCTCCCAGCGAGCCCTGGACCTCTC 842
                                                                                                                                                                                                             CB554607 SMSP Macaca mulatta cDNA, mRNA seguence.
                                                                                                          CGAGCGGAGAACAGGCTT-GCTCCCAGCAGCGAGCCCTGGACCTCTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tags from Rhesus macaque spleen Unpublished (2002)
Contact: Holzman T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Mashington
Box 358070, Saattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
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/dev_stage="adult"
/clone_lib="MMSP"
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Macaca mulatta
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/db_xref="taxon:9544"
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Best Local Similarity 94.2
Matches 467; Conservative
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EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 04-SEP-2003
                                                                                                                                                                 399 CACTCAAGCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTT 458
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Famil s.wiemanG&Kfz-heidelberg.6e;
sequenced by GBF (National Research Centre for Bictechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
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/dev_stage="fetal"
/dab_nost="DH108"
/clone_lib="779" (synonym: hncc1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 ATCAAAGAAGAAACAGAAAAAGCAGCATCAGTTGCCCAGTTTCCCAGAACCCAAATGATC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 514)

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This clone (DKFZp779N169) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenbug, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1722 ATCAAAGAAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATC
                                                                                                                               1782 CACTCAAGCCCCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 Argeracridecacrideriderecrederideridecedereceaegrecondecrargeargaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX470328 514 bp mRNA linear BST 04-SE
DKFZp779N169_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
DKFZp779N169_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.0%; Score 421; DB 5; 97.7%; Pred. No. 2.3e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779N169"
                                                                                                                                                                                                                                                                                                                                                                                 1902 AGAAGTCAAGTTCCAA 1917
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us-09-937-636-2.rst

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library in pSport1 to biotinylated RNA transcribed from
the driver, A44.1neg cDNA library in pSport2 with inserts
cloned in the complementary orientation. For detailed
protocols and additional information please see our
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Fetal Liver; Vector: Sport 1; Site_1: Sal 1; Site_2: Not 1; Two directionally cloned coba libraries were made from fetal liver hematopoietic stem cells enriched to be Lineageneg/lo, AA4.1pcs, cKitpos, Ly6A/E (Scal)pos called Scapos and from AA4.1ncg fetal liver cells. Subtractive hybridization was performed by hybridization of the target, Scapos, single stranded CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1094 TCACCTGCCACGCTCGGCACCCACTGGGCTCCCCAGCGTCTCTCAGCCTCTCCGTGC 1153
                                                                                                                                                                                                                         Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
Tel: 609 258 2838
Fax: 609 258 2759
                                                                                                                                                                                                                                                                                                                                                             enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAAGCAGAGAATAGGCTGGGCTCCCAGCAACATACCCTGGACCTCTCTGTGCTGTACC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            854 CTCCAGAGAACCTGAGAGTGATGGTTTCCCQAAGCAAACAGGACAGTCCTGGAAAACCTTG 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 GGAATGCCATCTCCCTCCCAGTCCTGGAGGCCAAAGCCTGTGCCTAGTCTGTGTCACCT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Hematopoietic"
/cell type="Stem Celis; Lineageneg/lo, AA4.1pos, cKitpos,
Ly6A/E (Sca-1)pos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                   Email: ilemischkä@molbio.princeton.edu
These ESTs are derived from a subtracted cDNA library enriched fo
gene products expressed in day 14-14.5 fetal liver hematopoietic
stem cells defined as Lineageneg/lo, AA4.1pos, cKitpos, LyGA/E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'clone_lib="Hematopoietic Stem Cell Subtracted Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734 CTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGGATTCAGGGCGCTACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ceadaaccerdecachadaderecerdegerdaaagerdegeacrergeacachadaerr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protocols and additional information please see our website at http://stemcell.princeton.edu."
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The genetic program of hematopoietic stem cells Science 288 (5471), 1635-1640 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev stage="Embryonic day 14-14.5"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Mus musculus"
                                                                                                                     Contact: Lemischka, Ihor R.
Department of Molecular Biology
Princeton University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: M13Reverse or T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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|Best Local Similarity
|Matches 497; Conserv
                           TOURNAL FINE FURMED COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                            1334 CCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGCTGTGAGG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠.
د.
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                                                                                                                                                                                                                                                                                                                                                             602 TCAANAGCTCCTGAAGCTCCTTTCAGGAGCTGGGGGCCANCCTTGGCTNACNTTTGAAGT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX345667 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI025YC24 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1011)
1 ("A" B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR vites of the pCMVSPORT 6 vector. Library was normalized.
1154 ACTACTCCCCGAAGCTGCTGGGCCCCTCCTGGTGCTGGAGGCTGAGGGTCTGCACTGCA
                                                                                                                                                    482 ACTGCTCCTCCAGAGCCTGGCCTGCCCCTTCCTGCGCTGGCGGCTGGGGGAAGGGGCTGC
                                              422 ACTACOCGCCCCAGATGTCCAGCCCCTCCTGGGAGGCCAAGGGTCTGCACTGCA
                                                                                                   1214 GCTGCTCCTCCCAGGCCAGCCCGGCCCCTCTCTGGCGTGGCTTGGGGAAGAGCTGC
                                                                                                                                                                                                                                                          542 TGAAGGGGAACAGCAGCAATGCCTTCTTTCACAGTCACTTTCAGCTCACTTGGACCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAI025BB12QP1&c=9384.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003 this sequence version replaced gi:30373021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1025YC24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX345667.2 GI:46290734
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                               CCTGGAA 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 CCTGGAA 668
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
BX345667
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KEYWORDS
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SOURCE	REFERE AUTH TITL JOUR COMMEN		FEATUR		ORIGIN Quer Best Aatc Qy Db Db	90 PP PP
<u> </u>	,					
62 TCTGGATACGAGTGCAGGAGTCAGTGATGG-TGCCGGAGGGCCTGTGCATCTCTGTGCCC 120	TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGGTACTGGGTACTGGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGCTTATTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGTACTGGAGTACTGGTACTGGTACTGGTACTGGTACTGGAGTACTGAAACCACTGAAACCACCAAAGACTCGTATGGCCACAAACCACCAAAGACCGGTACTGTAGGCCACTAACAACCAAAGACCGGTACTGTACAAACCAAACAAA	241 GAGGTGGAATGAGCACCGGGGCCGATTCCAGCTGACGGGAACCCCCAAGGGGAAC 300 273 GAGGTGGAAATGAGCACCCGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAC 330 273 GAGGTGGAAATGAGCACCCGGACCGACACTCCACTGGGGATCCCGGCAAAGGGAGC 332 301 TGCTCCTTGGTGATCAGAGACGCGCAGATGAGTGAGTCACAGTACTTCTTTCGGGTG 360 333 TGCTCCTTGGTGATCAGAGACGCGCAGAGGGAGGATGAGACACATCTTTCGGGTG 360 361 GAGAGAGCAAGCTATGTGAGATAAATTTCATGAGGATGATCTTTCTAAAAGTAA 418 361 GAGAGAGGAAGCTGTGTGAGATAAATTTCTGAGGGTTCTTTCT	419	513 ACGGTCATCTGTGTGTTTAACTGGGCTTTCAAGAAATGTCCAGCCCCTTCTTTCT	487 AGAAAGGETGAGGCACAGAGGACCGTCCGTGTGGCCTATGCCCCCAGAGAC 546  [1]	925 TRGGGSCMCMGAACCCTGGGGSTCGARCTGCGTGGGGTACGGGCGGGGATTAMGGGGCAC 984 787 TACACCTGCCGAG 799 985 MCYTGCGASSGAG 997
Sy Dp	oy og de	868686	8 B 8	9	8 8 8 8 8 8 8 8	9 5 Q

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CCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCCTGCAGCTGCCAGATAAGAAGGGAC 1453
181 recadedadadedadedadedecrectreaadereacerecadereaceredadedededed
                                                                                     241 CCAACAGCTCCCTGAGCCTCCTTCAGGAGCTGGAACCCAGCCTCTGGCTCAGCTGTGAAG 300
                                                                                                                                                            CCAACAGCTCCCTGAGCCTCCATGGAGGCCTCAGCTCCGGCCTCAGGCTCCGCTGTGAGG
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                                             à
                                                                                COS55499 810 bp mRNA linear EST 19-JUL-2004
AGENCOURT 28542322 NIH_MGC_249 Rattus norvegicus cDNA clone
INAGE:7375918 5', mRNA sequence.
COS555499 GI:50367692
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RESULT 13 CO555499 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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Rattus.

Exercises 1 to 810)

MIF-MGC http://mgc.nci.mih.gov/.

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Outract: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

College of Misconsin

Misconsin Misconsin

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                                  Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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1 Similarity 71.3%; Pred. No. 5.4e-76;
506; Conservative 0; Mismatches 190; Indels 14; Gaps
Rattus norvegicus (Norway rat)
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61 ACTACCCCACACAGATGTCCAGACCCTCCTGCTCCTGGGGATTCTGAGGGTCTGCACTGCA

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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1634 CGGCTGGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCCACAACAACAGTCCTCGGACCC 1693
                                                                                                                                                                                                                         CCCCGAGGCCCAGGTTCTCCCGGCACAGGACGATCCTGGATTACATCAGATGGGTCCCGA 1633
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keele,J.W.

Porcine gene discovery by normalized cDNA-library sequencing and
     1454 TCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 AGACCAGGTCCCCCGCT-----CGGAATTGGAAAGCTGAAACCAGACACCCCTTCTGGGA
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4396
Fax: 402 762 4390
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Mamm. Genome 13 (8), 475-478 (2002)
22213789
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Plate: 139 row: G column: 10
Seq primer: ATTTAGGTGACACTATAG.
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Mus musculus
Mus musculus
Eukaryota, Musculus
Eukaryota, Musculus
I (bases 1 to 580)
Marram. Hillier.L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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AA764005

BEN 27-JAN-1996

WRNA linear EST 27-JAN-1996

WOSG402-II Soares thymus 2NNM musculla cONA clone

IMAGE:1243299 5' similar to SW:MAGS MOUSE P16880 WYELIN-ASSOCIATED

GLYCOPROTEIN, SHORT FORM PRECURSOR 7, MENA sequence.
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Contact: Marka M/Mouse EST Project
Washd-HHMI Mouse EST Project
Washd-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Prorest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousees@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                       190 GAAAGCTTCGGGAATTGCACATCCATCCGGTCCTGGAGGGCCAAAGCCTGCGTCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1144 CTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCGAGGCTGAGGGT
                                                                                                                            844 GTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAAGCAAACAGGACAGTCCTG
                                                                                                                                                                                                                                                                                                                                                                         904 GAAAACCINGGGAACGGCACGICTCICCCAGIACTGGAGGGCCAAAGCCTGTGCCTGGTC
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2.8e-72;
ches 95;
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High quality sequence stop: 503.
     Pred. No. 2.8e
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          80.4%;
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  Best Local Similarity
Matches 390; Conserv
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AUTHORS
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🖍 Query Match

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943 GGCCAAAGCCTGTGCCTGTCTGTCACACACAGCGCCCCCCCAGCCTGAGCTGG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1003 ACCCAGAGGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCCAGCC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 CTGGAGCCCCAGGGAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----cagacingcangaarccincacarciggaagincagcaaggccagicrcir 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643 CGGCTCCTCTGTGCTGCTGACAGCCAGCCCCTGCCAACTGAGCTGGGTCCTGCAGAAC 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 AGAGTCCTCCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGGCTGGAGCTGCCCGGG 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 CAAGCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAG 942
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                                               organism="Mus musculus"
                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:1243299"
                                                                                                                                                                               tissue_type="Thymus"
/dev_stage="4_weeks"
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                                                                  "mol_type="mRNA"
'strain="C57BL/6J"
                                                                                                                                                            sex="male"
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Best Local Similarity
Matches 428; Conserv
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FEATURES
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1 atgctactgccactgctgct......atgcagaagtcaagttccaa 1917
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaa37848 Human obe	Aav99912 Human sia	Aav99911 Human sia	Aaa80610 Human CD3	Ada27034 Human nov	Ade86564 Novel hum	Abk43361 DNA encod	Abk43367 DNA encod	Abk43373 DNA encod	Adi37009 Novel hum	Adl82804 Human PRO	Ada27152 Human nov	Add19239 Human cDN	Abk43362 DNA encod	Abk43360 DNA encod	Aaz34109 Human PRO	Aac78510 Human PRO	Aas45983 Human DNA	Aca63677 Novel hum	Aca89433 cDNA enco	Aca73443 Human sec
SUMMARIES	QI	AAA37848	AAV99912	AAV99911	AAA80610	ADA27034	ADE86564	ABK43361	ABK43367	ABK43373	ADI37009	ADL82804	ADA27152	ADD19239	ABK43362	ABK43360	AAZ34109	AAC78510	AAS45983	ACA63677	ACA89433	ACA73443
	DB	m	N	~3	m	σ,	12	v	G	G	12	12	σ	10	ဖ	G	~	m	4	œ	α	ω
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	% Ouery Match	100.0	100.0	100.0	99.2	99.5	99.2	97.4	90.4	90.4	90.5	90.2	90.2	89.8	78.1	69.7	9.69	9.69	9.69	9.69	9.69	9.69
	Score	1917	1917	1917	1907.4	1907.4	1907.4	1868	1733	1733	1729.8	1729.8	1729.8	1721	1497.4	1337	1333.8	1333.8	1333.8	1333.8	1333.8	1333.8
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Aca05758 Human sec	$\sim$		Acf19553 Human sec	Acd21841 Human sec	Acf13006 Human sec	0	8 Human	Novel	Acd04739 Novel hum	Acd18200 Human sec	Acd08207 Human sec	Aca88641 Novel hum	0083 Human	Acd12305 Novel hum	Acc74220 Human sec	Acd15848 Human sec	Acd25416 Novel hum	Acd17893 Human sec	$\neg$	Acd21534 Human sec	9	Aca71841 Human sec	Abx98211 Human cDN
8 ACA05758	ACA6659	8 ACF20167		8 ACD21841	8 ACF13006		8 ACF00158	8 ACA72215	8 ACD04739	8 ACD18200	8 ACD08207	8 ACA88641	8 ACA70083	8 ACD12305	8 ACC74220	8 ACD15848		8 ACD17893	8 ACC88180		Æ	8 ACA71841	8 ABX98211
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1333.8		1333.8	m	m.		ω.	m.	۳.	m.	m	m.	m.	m.	m.	1333.8	ω.	ω.	٠	ω.	۳.	m.	۳.	1333.8
22									31				35		37		<u>გ</u>		41	42	43	44	45

## ALIGNMENTS

This sequence encodes a human obesity protein binding protein-2 homologue (hob-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity, related disorder; therapy; ds. Human obesity protein binding protein-2 homologue coding sequence #2. New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders. Location/Qualifiers
1. .1917
/\*tag= a
/product= "hOB-BP2h" BP. Claim 3; Page 86; 92pp; English. 02-APR-1999; 99US-0127667P. AAA37848 standard; DNA; 1917 22-MAR-2000; 2000WO-US006682. (first entry) (ELIL ) LILLY & CO ELI. WPI; 2000-664992/64. P-PSDB; AAY97543. WO200059942-A2. Su EW, Wei J; Homo sapiens 12-OCT-2000. 12-FEB-2001 AAA37848; RESULT 1 AAA37848  us-09-937-636-2.rng

are or obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids a wiseful as probes or amplification primers in the detection, advantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides 

Sequence 1917 BP; 411 A; 627 C; 532 G; 347 T; 0 U; 0 Other;

ery M	Match	100.0%; Score 1917;		
ist Lches	cal 191	Pred. No. 0; 0; Mismatches 0; Indels 0;	Gaps 0	٥ ;
	т н	1 ATGCTACTGCCACTGCTGTGTCTCGCTGCTGCGGGGGGTATGGATGG	AGA 60     AGA 60	
. 42	61	61 TTCTGGATACGAGTGCAGTGATGATGCTGCCGGAGGCCTGTGCATCTCTGTGCCC	GCC 120     	
	121	21 TGCTCTTTCTCCTACCCCGACAAGACTGGACGGGTCTACCCCAGCTTATGGCTACGG	TGG 180	
	181	81 TICAAAGCAGTGACTGACAACCAAGGGGCGCTCCTGTGGCCACAAACCACCAGAGTCGA 	CGA 240	
r, julija,	241 241	41 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGAAAC 	AAC 300       AAC 300	
2 1 4	301	01 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG	GTG 360      GTG 360	
	361 361	51 GAGAGAAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	ACA 420     ACA 420	
	421	21 GTGGTCAGGTTCACGCCCAGACCCCAGACCCCAACCTCACCTGCCATGTGGCCACGTGTGGCCATGTGGACC21 GTGCTCACCTGCCCTGCCATGTGGAC	GAC 480      GAC 480	
	481	1 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCCACTCCGTGTGCCCTATGCCCCCCGT	CCC 540	
,	541 541	11 AGAGACCTTGTTATCAGCATTTCACGTGACAACGCCAGCCCTGGAGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCAGCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCCAGGCCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCAGCCCCCAGGCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCC	CAG 600       CAG 600	

1020 1080 1080 1140 1140 1200 1260 1260 1320 1320 1380 1380 1020 1440 1440 1500 1560 1560 1200 1620 1680 1680 1740 1740 1800 1800 1860 1500 1620 096 CAGGAGAGCCAAGAGCACCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1860 900 CCTGAGGCCCGGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917 CCTGAGGCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAGATCAAGTTCAA 1917 1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCACTCAAGCCCCAGAATCC CTGGADAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 1021 creaccecreceaccereaccecegesereresacresereresacreserreasers CACGAAGGAGGTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTC AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCTGAG GCCGGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGG 1441 GATAAGAAGGGACTCATCTCCAACGGCATTCTCCAACGGAGCCTTTCTGGGAATCGGCATC ACTCAGACAGAAACCCCGAGGCCCAGTTCTCCCGGCACAGCACGATCCTGGATTACATC AGTOCTOGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA AGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG GTCTGTGTCACACACACAGCCCCCCAGCCAGGCTGAGCTGGACCCCAGAGGGACAGGTT CTGAGCCCCTCCCAGCCCTCAGACCCCGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG <u> GGT CTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCCTCTCTGCGCTTGGTGGTTT</u> GGGGAGGAGCTGCTGGAGGGGAACAGCAGCAGGACTCCTTCGAGGTCACCCCCAGCTCA GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA GCCGGGCCCTGGGCCACACAGCTCCCTGAGCCTCCATGGAGGGCTCAGGCTCCGGCCTCAGG GATAAGAAGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC ACGGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG ACTCAGACAGAAACCCCGAGGCCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATC AATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACAAAC AATGTGGTCCCGACGCCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAAC AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCACAG 1021 1141 1261 1501 1561 1621 1681 1741 841 196 1081 1081 1201 1201 1261 1321 1381 1381 1441 1501 1561 1621 1681 1801 1801 106 901 961 1141 1321 1861 1861 ò qq à 쉱 ò 셤  $\dot{\delta}$ g  $\dot{\delta}$ 음 8 엄 ठ g 임 дq q q ŏ ð ò à 8 셤  $\dot{\delta}$ 음 ò 셤 Š 임 g à à g

RESULT

841 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 900

GGGCGCTACACCTGCCCGAGCGGAGAACAGGCTTGGCTCCCCAGCAGCGAGCCCTTGGACCTC

600 999 999 720 720 780 780 840 840

601 GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT GACAGCCAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC GACAGCCACCCTGCCACACTGAGTCTGAGTCTGCAGAAACAGAGTCCTCTCCTCGTCC CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA 721 CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCGGGGTGAAGGCTGGGGATTCA GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTC

661

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721 661

781 781

GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT

541 601

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51. .4***
/*tag= a
/transl_except= (pos:1176. .1177, aa:Pro)
/note= "this codon has an apparent 1 nucleotide deletion
which alters the reading frame"
                                                                                               SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmuse disease; allergy; asthma; inflammation; cerebellar autoimmuse disease; allergy; asthma; inflammation; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischemia reperfusion injury; cardiovascular disease; Kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AlDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New sialoadhesin family 4 polypetides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.
                                                                           Human sialoadhesin family 4 (SAF-1) related EST clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 31-32; 48pp; English.
                                                                                                                                                                                                                      Location/Qualifiers
51. .1249
            AAV99912 standard; cDNA; 3099 BP.
                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                            Erickson-Miller CL;
                                                                                                                                                                                                                                                                                                                                                                 97US-0047572P.
                                                                                                                                                                                                                                                                                                                                             98WO-US010791.
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-080779/07.
P-PSDB; AAW81024.
                                                                                                                                                                                                                                                                                                                                             27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1997;
                                                     26-APR-1999
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                 WO9853840-A1
                                                                                                                                                                                                                                                                                                                       03-DEC-1998,
                                                                                                                                                                                                                                                                                                                                                                                                             Kikly KK,
                               AAV99912;
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This is the nucleotide sequence of an expressed sequence tag (EST) clone that encodes a polypeptide (see AAM81024) which shows close homology cand/or structural similarity (e.g. a conservative amino acid difference) to new human sialoadhesin family 4 (6.8F-4) polypeptide (see AAM81023).

SAF-4 polynucleotides and polypeptides, and methods for producing such colypeptides in transformed host cells using recombinant techniques, are disclosed in transformed host cells using recombinant techniques, are disclosed that enhance or inhibit SAF-4 expression, may be used to treat coloring that enhancement or inhibit in the search of activity. Conditions that may benefit from such treatment include cancer, inflammation, cerebollar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury canage and other neurological discorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, mycoraciala inflammage and other neurological discorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, mycoraciala infarction, hypotension, 
Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;

Query N Best Lo Matches	Match Local les 1917	100.0%; Score 1917; DB 2; Length 3099; Similarity 100.0%; Pred. No. 0; 7; Conservative 0; Mismatches 0; Indels 0; Gaps	,0
δλ	1	TACTGCCACTGCTGCTCGTCGCTGCTCGCGGCCCCAGGCTATGGATGG	0
qa	51	TGCCACTGCTGCTTCTTCGCTGCTGGGCGGGTCCCAGGCTATGGATGG	10
ò :6	61		50
9 6	131	CIGGATACGAGGGCAGGAGGCAGGCAGGGGCCGGAGGGCCCIGIGCAICLICIGIGCCCIGIGCAGGGCCCIGIGCAGAGGCCCCIGIGCAGAGGCCCCIGIGCAGAGGCCCCIGIGCAGAGGCCCCCIGIGCAGAGGCCCCCCCC	
<u> </u>	1 1		
<i>&amp;</i>	œ		
වු	231	ACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 2	06
상 · 원	241	GAGGTGGAAATGAGCACCCGGGGGCCGATTCCAGCTGACTGGGGATCCCGCCAAGGGGAAC 30	00
ŏ		ATCAGAGACGCGCAGGATGCAGGATCACAGTACTTCTTTCGGGTG 3	
QD	351		10
\chi_{\text{c}}	361	ATAATTICATGAACGATGGGTTCTTTCTAAAAGTAACA 4	7 70
2 (	- 0	AGAGAGGAAGCAALGIGAGALALAALIIICAALGGAALGG	
S S	421	GTGCTCAGCTTCACGCCCAGACCCCAGACACACACACCACCTCACCTGCCTG	30
ò	481		40
qq	531	zadadadegrerendadegeacadadadegecegecederecegecegesecedes	06
δγ.	4		00
Dp	591	CCTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCCAGCCCCA	
<u>ک</u> دو	601	GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGGGTCCTCTGTGCTGCT 66	09 -
g è	n u	11GICCCATACCIGGAAGCCCCAAAAAGGCCAGIICCIGCGGCICCICCICTGGGGCIGCI	0 6
S &	ρ ⊢	GACAGCCAGCCCCTGCCACACTGAGCTGGGTCTGCTGCAAAAAAAA	
ò	721	CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA 78	80
DP	771	CTGGGGCCCTAGACCCCTGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGTTTC	30
Qy	781	GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCAACCCTGGACCTC 84	
QD	831	oderacacerdeceadeddaaaadaddecreecadeadaddaadecerddaecer	06
ογ	841	TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 90	00
QC C	891	ctgrecagtatcrccagagaacctgagagtgatggttrcccaagcaaacaggacagt	20
δy		TGBAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 96	0
DP DP	951	GGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 10	-
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AAV99911 standard; cDNA; 3099 AAV99911; RESULT 3 14V99911

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26-APR-1999

(first entry)

Human sialoadhesin family 4 (SAF-1) cDNA

SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease;

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polypoptide (see AAWB1023). It can be obtained e.g. from a cDNA library derived from mRNA in cells of human primary dendritic cells using derived from mRNA in cells of human primary dendritic cells using derived from mRNA in cells of human primary dendritic cells using methods for producing such polypeptides by recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4 expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, carebellar degeneration, Astheimer's disease, Parkinson's disease, multiple sclerosis, astheimer's disease, Parkinson's disease, multiple sclerosis, amountophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, acceptance of the separativities, ischemia reperfusion injury morardial ö 120 170 180 11:0 disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes and other haematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity Methods of identifying agonists, anatagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAF-4 activity or multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarchritis; ischemia reperfusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AlDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss. TGCTCTTTCTCCTACCCCCGACAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG Treregaraceagracagagreagrangaragracegaggsecrargearerererere TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG t O TTCTGGATACGAGTGCAGGAGTCAGTGATGCTGCCGGAGGGCCTGTGCATCTCTGTGCCC Gaps New sialoadhesin family 4 polypetides and polynucleotides - useful treat various diseases associated with SAF-4 expression. cDNA clone codes for new human sialoadhesin family 4 (SAF-4) .. Length 3099; Sequence 3099 BP; 769 A; 908 C; 813 G; 607 T; 0 U; 2 Other; Indels .; 0 DB 2; .. 0; Mismatches 100.0%; Score 1917; 100.0%; Pred. No. 0; Location/Qualifiers Claim 2; Page 30-31; 48pp; English. (SMIK ) SMITHKLINE BEECHAM CORP. ij 97US-0047572P. Best Local Similarity 100.0%; Matches 1917; Conservative ( 98WO-US010791 Kikly KK, Erickson-Miller 51. .19 /\*tag= WPI; 1999-080779/07. P-PSDB; AAW81023 27-MAY-1997; sapiens WO9853840-A1 03-DEC-1998. 61 111 121 Query Match evels. Ното Key ò g ò q ò

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	AAA80610 standard; cDNA; 2295 BP.  AAA80610;  AAA80610;  21-NOV-2000 (first entry)  Human CD33-like secreted protein gene #5.  Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; anticancer; vulnerary; antiviral; antibacterial; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; imflammatory arthritis; dermatible sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; rheumatory disorder; inflammatory bowel disease; crohn's disease; rheumatory disorder; inflammatory bowel disease; crohn's disease; rophritis; hyperprofilerative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; ss.  WO200029435-A1.  25-MAY-2000.  27-OCT-1999; 98US-0105971P.
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181   TTCAAAGCAGTGACTGAGAGGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 240   1   1   1   1   1   1   1   1   1	1

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(HUMA-) HUMAN GENOME SCI INC

Υ; Wei Kenny JJ, Moore PA, Young PE, Ruben SM, Olsen HS, Greene JM, Ni J,

WPI; 2000-387742/33.

Asolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases. P-PSDB; AAB25580

Claim 1; Fig 13A-C; 803pp; English.

AAA80666-A80623 encode the 12 secreted protein sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in AAB25576-E25593. The buman secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiatrinitic; antirheumatic, dermatiological; antiproliferative; antiatrinitic; antirheumatic, dermatiological; antiproliferative; and antiatrinitic; anticoner; various disease, antiagonists may be used to treat prevent and/or diagnose various disease, disorders may be used to treat prevent and/or diagnose various disease, disorders may be used to treat prevent and/or diagnose various disease, disorders may be used to treat provent and/or diagnose various disease. Addison's disease, rheumatory disorders e.g. inflammatory bowel disease, cronnary acterioscierosis and myocarditis; hyperproliferative disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #5 and protein sequences are represented in sequences AAA806610 and AAA806580. Sequences are represent genes related to the present invention relates to 12 secreted human proteins and the secreted protein gene#5 

Sequence 2295 BP; 494 A; 732 C; 620 G; 449 T; 0 U; 0 Other;

ö 180 240 TICTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120 177 237 297 300 IGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360 417 477 480 Argeracreccacrecrererecreerecreeredecedereccaderargaridadada 117 GAGGIGGAATGAGCACCCGGGCCGATICCAGCICACTGGGGATCCCGCCAAGGGGAAC 357 TTCAAAGCAGTGACTGAGACAAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA recretriterecrececeaeaaaacresacassereraceceaserrareseracies TTCTGGATACGAGTGCAGGAGTCAGTGGTGCCGGAGGCCTGTGACATCTCTGTGCCC TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA 241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 358 recreeringerdarcadeagacececagargeaggargaercacagracrecritegere 421 GTGCTCAGCTTCACCCCAGACCCCAGACCACAACACCGACTCACCTGCCATGTGGAC 0; Gaps Score 1907.4; DB 3; Length 2295; Pred. No. 0; Indels 9 Pred. No. 0; 0; Mismatches 99.5%; 99.5 Best Local Similarity 99.7 Watches 1911; Conservative 28 61 118 178 238 298 301 121 181 361

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M, Liu D, Crocker PR;
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19-APR-2000, 2000US-0198407P.
30-0CT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836353.
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The invention relates to an isolated nucleic molecule that is at least SX The invention relates to an isolated nucleic molecule that is at least SX dentical to 18 human cDNA sequences representing 12 novel genes according secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridise under stringent conditions to a nucleic acid molecule conditions to a nucleic acid molecule capable of having a polyperide sequence of any A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide fragment, domain, epitope, it is alleast 95% identical to a polypeptide fragment, domain, epitope, it is included are recombinant vectors, not the polypeptide fragment, domain, epitope, it is consistent and polypeptide fragment, domain, epitope, it is included are specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptides, diagnosing, treating, preventing specifically propertied, the gene corresponding to the cDNA sequence and activity, in a biological assay (by expressing the polynucleotide or dientifying an activity). The polypeptides, moleic acids and antibodies are useful for diagnosing a pathological condition, such as cancer, inflammation or a susceptibility to a pathological condition, such as cancer, inflammation and other immune disorders, nucrological and blood clotting disorders (many axamples are restriction mapping). The polypeptides and antibodical condition, such as cancer, inflammation and other immune restriction, radiation hybrid mapping or long-range restriction mapping). The polypeptides and antibodication of the restriction mapping the polypeptides and antibodication of the restriction mapping the polypeptides and antibodication of the
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                             The invention relates to an isolated nucleic acid sequence, or its stalelic variant, a fragment of the cDNA sequence, or its fragment domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver discorders such as hepatitis or neural disorders such as Albheimer's disease. The present sequence represents cDNA encoding a novel human secreted protein.
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                                                                                                                                               Sequence 2295 BP; 494 A; 732 C; 620 G; 449 T; 0 U; 0 Other;
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                                                                                                                                                                          Length
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Pred. No. 0;
0; Mismatches
     NO 15; 380pp; English
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ilarity 99.7%;
Conservative
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Best Local Similarity
Matches 1911; Conser
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DNA encoding stalic acid-binding Ig-related lectin, Siglec-BMS-L3b
                                                                                                                                                                                                                                                                                                                  Human; stalic acid-binding Ig-related lectin; SIGLEC; asthma; mimune system disease; leuksemia; allergy; inflammacory disease; tissue damage; allergic rhinitis; ostecarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.
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                                                           ABK43361 standard; cDNA; 2954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000US-0220139P
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P-PSDB; AAU87075.
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ABK43361

ABK43361

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The invention relates to an isolated SIGLEC (stalic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) related lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) to passays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's inhibit inflammation diseases such as allergic rhinitis, osteoarthritis, Crohn's inflammatory diseases such as allergic rhinitis, osteoarthritis, also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS on biological sample. (II) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC-BMS antibodies associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also useful sequences and PCR primers of SIGLEC-BMS proteins and in diagnostic imaging technology. Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, weukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

9. 10. ਨੇ q ò g  $\delta$ g  $\delta$ qq 8 qq ð

Sequence 2954 BP; 715 A; 869 C; 780 G; 590 T; 0 U; 0 Other;

ö 169 9 1 TGGATGGGAGATTCTGGATACGAGTGCAGTGAGTGATGATGATGGAGGGCCTGTGCA TGGATGGGAGATTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCA TCTCTGTGCCCTGCTCTTTCTCCCTACCCCCGACAGACTGGACAGGGTCTACCCCAGCTT Gaps . DB 6; Length 2954; Indels ö 97.4%; Scor. 100.0%; Pred. No. v. ... 0; Mismatches Conservative Query Match Best Local Similarity Best Local Sim 110

8 B

TCTCTGTGCCCTGCTCTTTCTCCCTACCCCGGACAGGACTGGACAGGGTCTACCCCCAGCTT

1069 1020 1129 529 480 1080 649 720 1189 240 349 420 589 0.09 829 840 949 289 300 409 360 469 540 709 099 769 960 CCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAA 889 841 ACAGGACAGTOCTGGAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAA 900 ATGGCTACTGGTTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACC eccardregacricicagaaagggrergagggggggaggaggacggrergg TCTCCTCGTCCCATCCCTGGGGCCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGGTGAAGG CCCTGGACCTCTCTGTGCAGTATCCTCCGAGAAACCTGAGAGTGATGGTTTCCCAAGCAA ACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGGCCAAA 1010 GGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGGTCCTGGAGCTGCGTCGGG GGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGGTCCTGGAGCTGCTCGGG 1141 GGGAGGCTGAGGGTCTGCACTGCAGCTGCTCCTCCCCAGGCCAGCCCGGCCCCCTCTCTGC ACCAGAGTCGAGGGGGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCG 181 ACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCG 241 CCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACT TCTTTCGGGTGGAGAAGCTATGTGAGATATATTTCATGAACGATGGGTTCTTTC TAAAAGTAACAGTGCTCAGCCTCAGGCCCAGGACCCACAACACCGACCTCACCT GCCATGTGGACTTCTCCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGG CCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCC TCTGTGCTGCTGAGCCCCCTGCCACACAGTCCTGGGTCCTGCAGAACAGAGTCC TCTGTGCTGACAGCCAGCCCCTGCCACACACAGGCTGCTGCTGCTGCAGAACAGAGTCC TCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGCGGCTGCCCGGGGTGAAGG CTGGGGATTCAGGGCGCTACACCTGCCGAGCGGGAGACAGGCTTGGCTCCCAGCAGCGG crassearreaseceracacerdeceaseceaseacaserresereceasease 901 decrerecreerererereacacacacacecececasecasecreasecres 1081 ACGICITCICAGCCICICCGIGCACIACICCCCGAAGCIGCTGGGCCCCTCCTGCTCCT GGGAGGCTGAGGGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGC CCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACT TCTTTCGGGTGGAGGAAGGTATGTGAGATATAATTTCATGAACGATGGGTTCTTTC TAAAAGTAACAGTCCAGCTTCACGCCCAGACCCCAGGACCACACACCCGACCTCACCT CCTATIGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGC cccadecccadegaanereccaraceresaageecaaaaageeree 1070 TICAAGIGGAGGACGAAGAAGAGATTCACCIGCCACGCICGGCACCCACTGGGCICCCAGC 1130 ACGICTCTCTCAGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCT 170 121 230 301 410 421 830 890 290 350 361 470 530 290 650 710 661 270 950 541 781 1021 1190 721 601 961

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1489
  1549
  1560
  1729
  1909
   1429
   1440
   GAATCGGCATCACGGCTCTTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTAC 1500
   CGAAGAGACGGACTCAGACAGAACCCCGAGGCCCAGGTTCTCCCGGGCACAGGATCC 1609
   TGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAG 1669
   ccacaccaaacagrecregaccecrerrecaccagagerecrecereceagaarcaaaga 1680
  AGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCACCACAAG 1740
   TCAGACCCAGGCCTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCA 1860
   AGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAG
   CCCCAGAATCCCAGGAGACCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCG
   CCCCAGAATCCCAGGAGAGCCAAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCG
  TCAGACCCAGGCCTGAGGCCCCGGATGCCCAAGGGCACCCAGGGGGGATTATGCAGAAGTCA
   Tecaecreccaearaagaageacrcarcrcaacegcarrcrccaacegagegrrrcred
   TGCAGCTGCCAGATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGG
  cgaagagaggactcagacagaaaccccgaggcccaggrrcrcccggcacagacaca
  CCCCCAGCTCAGCCGGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGAAGGCCTCAGCT
  Human, sialic acid-binding Ig-related lectin, SIGLEC, asthma, immune system disease, leukaemia, allecyj, inflammatory disease, tissue damage, allergic rhintis; osteoarthritis; Crohn's disease psoriasis; rheumatord arthritis; conjunctivitis; gene; ss.
   DNA encoding sialic acid-binding Ig-related lectin, Siglec-10
  GAATCGGCATCACGGCTCTTCTTTCCT
  ABK43367 standard; cDNA; 2208
  20-JUL-2001; 2001WO-US023082
   21-JUL-2000; 2000US-0220139P
   (first entry)
   1910 AGTTCCAA 1917
   AGTICCAA 1868
   WO200208257-A2.
  Homo sapiens
   05-JUN-2002
   31-JAN-2002
   1370
  1321
   1430
   1550
  1501
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow-companys, and imaging methods. (I) is useful as a target for drugs which inflammation, tissue damage and indicated in asthma, and continuity diseases such as allegic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS can be useful as mucleic acid molecules (II) are useful and biological sample. (II) are useful as mucleic acid probes or signed sample of signed some one of signed some one of signed some one of signed signed signed to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging bechnology.
   120
  180
   Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
   TICAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA
   TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC
  TECTCTTTCTCCTACCCCCGACAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG
   358 GAGGIGGAAAIGAGCACCCGGGGCCGAIICCAGCICACIGGGGAICCCGCCAAGGGGAAC
  TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG
  Arecracioccaciecrecrerecrescrescreses de arecras de arec
  Trengganacgagngeagenereanganggngeecggaggeerrengearetergeece
   recrerreceracececeacaacaecacacacaceceracececacerrarecerace
   TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGGCCACAAACCACCAGAGTCGA
   GAGGTGGAAATGAGCACCCGAGTTCCAGCTCACTGGGGATCCCGCCAAGGGGAAAC
   Gaps
  Indels 174;
   6; Length 2208;
  Sequence 2208 BP; 463 A; 737 C; 604 G; 404 T; 0 U; 0 Other;
   .
0
   DB
   Query Match
90.4%; Score 1733; D
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1917; Conservative 0; Mismatches
   Example 17; Fig 25; 209pp; English
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                              SQUIBB CO
  Whitney
                                  (BRIM ) BRISTOL-MYERS
  Ĥ
   WPI; 2002-241565/29.
P-PSDB; AAU87081.
   Chang
  Longphre M,
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| 6-2.rng                 | 1387 TGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC | RESULT 9 ABK43373 XX ABK43373 XX ABK43373 XX ABK43373; XX ABK43373; XX ASK43373; XX ASK43373; XX ASK43373; XX ASK43373; XX Buman; sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2. XX Human; sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2. XX Human; sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2. XX Human; sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2. XX Homo sapiens. XX Homo sapiens. XX XX Boro sapiens. XX XX Z1-JUL-2001; 2001WG-US023092. XX BRIN ) BRISTOL-WYERS SQUIBB CO. XX                                                                                                                                                                     |
|-------------------------|--------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Tue Nov 9 08:29:58 2004 | 19   19   19   19   19   19   19   19            | 947 CAGTATCCTCCAGAGAACTGAGAGTGATGCTAACCAACGACACTCCTGAAA 306 1138 CAGTATCCTCCAGAGAACTGAAGATGTTTCCCAAGCACAACGACACTCTGAAA 1197  907 AACCTTGGGAACGCACGTCTCTCCCAGTACTGAAGGCCTAAGCCTGTGCTGTTG 566 1198 AACCTTGGGAACGCACGTCTCTCCCAGTACTGAGGCCAAAGCCTGTGCTGTTG 1257  1198 AACCTTGGGAACGCACGTCTCTCCCAGTACTGAGGCCAAAGCCTGTGCTGGTTGT 1257  1198 AACCTTGGGAACGCACGTCTCTCCCAGTACTGAGGCCAAAGCCTGTGCTGGTTGT 1257  1198 AACCTTGGGAACGCACCCCAGCTGAGGTGGACTGGAGCTGTTGCTGGTTGT 1257  1107 ACCTTGCAACACACACCCCAGCTGGAGTGGACTGGAGCTGTTGAGCTGTTGTAAGCTGTTGAGC 1317  1108 GTCACACACACACACCCCAGCTGGAGTTGGAGCTGGAGTTCTAAGTGGAACACACAAA 1377  1107 CCCTCCCAGCCCTCCAGCTCGAGCTGGAGTTCCAGAGTTCTAAGCTGAAAAA 1377  1108 GGAGAGTTCACCTGCCAGGCTGGAGTTCCTGGAGTTCTCAAGCTCTTTAAGCTGAAAAAAAA |

The invention relates to an isolated SIGLEC (stalic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are inseful for treating immune system diseases such as asthma, lenksemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening diagnosis, prognosis, following inflammation, tissue dama end remodeling in asthma, and inaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue dama end remodeling in asthma, continctivities, croin as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nuclectide sequences and/or signed as signed as sample. (II) are useful as nucleic acid probes or secening genomic library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS nucleic BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

ABRA\$336-ABR\$4318 represent human SIGLEC coding sequences and PCR primers leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease. Example 11; Fig 6; 209pp; English 

Sequence 3024 BP; 699 A; 933 C; 790 G; 602 T; 0 U; 0 Other;

the invention

248 240 418 -----CAGTGCTC 426 188 TICTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120 180 recretriciceracecedadadacidadadacidacidacecedecinardeciadada GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCCCCAAGGGGAAC 300 gagenegaaaneageaeeeeggeeeanneeageneacheacheeganeeeaheeggaae 428 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360 recreerrances and a second and contract and a second a seco ----- 418 549 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG 608 ACGGICALCIGIGITITAACIGGGCCTITGAGGAAIGICCACCCCCTICTITCICCIGG 668 669 ACGGGGGCTGCCTCCTCCCAAGGAACCAACCAACGACCTCCCACTTCTCAGTGCTC 728 9 rrcresaraceastecaseastearearearesteceseasescererecarererere TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA Gaps 0; Indels 174; Score 1733; DB 6; Length 3024; 0; Mismatches Мо. Pred. Query Match
Best Local Similarity 91.7%;
Matches 1917; Conservative 249 189 361 489 129 61 121 181 309 241 369 301 429 419 419 g QQ dd a 유 8 8 ð g & à g ò g ò ò à ò

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received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, univial factors, differentiation factors, convival factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal: In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is a cDMA sequence which encodes a human PRO protein of the
   Best Local Sim:
Matches 1915;
  61
   181
  Query Match
   121
  218
  241
  278
   301
   338
   361
  398
  419
  458
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    1626
  GTCCCGACGGCTGGCTCAGAAGCGGAATCAGAAGCCCACAAACAGTCCT 1686
   1988
   1746
   1989 CGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAGCAG 2048
  1806
  2049 TATCAGTIGCCCAGITICCCAGAACCCAAAICAICCACTCAAGCCCCAGAAICCCAGGAG 2108
  1807 AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 1866
  2109 AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 2168
  'human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neropeptide; hormone; cell receptor; receptor-receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
   ACAGAAACCCCGAGGCCCCAGGTTCTCCCGGCACACCACGATCCTGGATTACATGTG
   ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCATCCTGGATTACATGATGTG
  CGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAGCAG
  TATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAG
  Wu T;
   GCCCGGATGCCCAAGGCCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917
   GCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 2219
  3
  Novel human secreted and transmembrane protein PRO 71236 cDNA
  Wood
  Schoenfeld J,
  /product= "Human PRO71236 protein"
  ŝ
  Location/Qualifiers
38. .2131
  Fong
   ADI37009 standard; cDNA; 2176
  Clark H, Dennis K,
   08-JUL-2003; 2003WO-US021083
   08-JUL-2002; 2002US-0394485P
  (first entry)
   /*tag=
   (GETH ) GENENTECH
  WO2004004649-A2
  Homo sapiens.
  22-APR-2004
  15-JAN-2004
   1567
  1869
  1929
  1747
                         1809
  1627
   1687
   1867
  ADI37009;
   2169
  Chiu H,
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157
  300
   120
   180
  217
  240
   277
   337
   418
  418
   418
   360
  397
   517
   426
  637
  577
  486
   697
  546
   757
  909
  7
  98 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC
  GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGGATCCCGGCCAAGGGGAAC
   GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG
  TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG
  158 recretificienacececeaeaacacacacacacacacececeaectrarecers
  TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA
  TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA
   GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
   TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG
  recreeringergarcagacececagarecagareagareagreacacagrerrerresesre
   -----CAGTGCTC
  AGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGACTTCTCC
   487 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC
  CTIGITATCAGCATTTCACGTGACAACACGCCCAGCCCTGGAGCCCCCAGCCCCAGGGAAT
   AGAAAGGGTGTGAGGGTGTACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC
   Gaps
                                  DB 12; Length 2176;
   2; Indels 174;
Sequence 2176 BP; 456 A; 709 C; 604 G; 407 T; 0 U; 0 Other;
                              90.2%; Score 1729.8; ilarity 91.6%; Pred. No. 0; Conservative 0; Mismatches
   Similarity
  547
  427
   638
   869
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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information

Claim 1; SEQ ID NO 9; 118pp; English

WPI; 2004-142912/14.

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P-PSDB; ADI37010

2017

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The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgM deficiency, selective deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkit's comparemediate lymphoma, intermediate lymphoma, tollicular lymphoma, tropermediate lymphoma, tollicular lymphoma, topermediated haemolytic hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic andemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondyiltis. The PRO proteins are also useful for preparing a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and commapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
   AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 2077
  New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
   Immunosuppressive, Cytostatic, Antiarthritic, Antirheumatic, Antianemic, Antialegic, Muscular, Neuroprotective, Nephrotropic, Antiinflammatory, Gene Therapy, PRO, B cell related disorder; cancer, immune-mediated inflammatory disease, human; gene; ss.
   CGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAGCAG
  TATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCCAGAATCCCAGGAG
   TATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAG
   AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG
   1917
   GCCCGGATGCCCAAGGCCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA
   Wood
   Fong S, Schoenfeld JR,
   BP
   Claim 2; Fig 6; 695pp; English.
   Human PRO71236 cDNA, SEQ ID 6.
   ADL82804 standard; cDNA; 2176
   Clark H, Dennis K,
   15-SEP-2003; 2003WO-US029097.
   16-SEP-2002; 2002US-0411392P
   (first entry)
  (GETH ) GENENTECH INC
  2004-329389/30.
   P-PSDB: ADL82805
   WO2004024097-A2.
  Homo sapiens.
  25-MAR-2004.
   17-JUN-2004
  2018
   1747
   2078
  ADL82804;
  1898
  1958
   1807
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   Chiu H,
   Wu ID;
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   1117
   1177
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   1357
   1417
  1477
  1597
   1657
   GTCACACAGGGCCCCCCCAGCCAGGCTGAGCTGGAAGGGGAAGAGGGAACAGGTTCTGAGC 1237
   1086
   AAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGGCT 1717
  CTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAG 1566
  GTCCCGACGCCTGCCTCCTGCTCAGAAGCGGAATCAGAAAGCCACAAACAGTCCT 1897
  TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGGACCCTGGACCTCTGTG 1057
  906
817
   999
   877
   726
  937
   786
  997
  846
  996
   ACAGAAACCCCGAGGCCCAGGTTCTCCCCGGCACACGATCCTGGATTACATGAATGTG
   cacrecadericereceadeceadeceadeceadecederereceadecerededad
   CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGC
  CCCTGGGCCAACAGGTCCCTGAGCCTCCCATGGAGGCTCAGCTCTGGCTCTGGCCTCAGGCTCCGC
  ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATGTG
  TOCGTGCACTACTCCCCGAAGCTGCTGCCCCCTCCTGCTCCTGGGAGGCTGAGGGTCTG
   receredactacrecesaacerecresececerecrecresereseasecreaseserere
  GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCAGCTCAGCCGGG
  cricitiricercrisecrisecersarcarcarsaasarreracsaasaasacses
  CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAA
  CAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAA
  AACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGTCTGT
   cerreceadecereaacecedagaerecragaacracereagarreaagragaacaeaa
   GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCAGCCGGG
   GTCCCGACGGCTGGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACAACAGTCCT
CITGITATCAGCATTTCACGTGACACACGCCAGCCCTGGAGCCCCAGCCCAGGGAAAT
   GTCCCATACCTGGAAGCCCAAAAAGCCCAGTTCCTGCGGCTCCTCTGTGCTGCTGCTGACAGC
   CAGCCCCTGCCACACTGAGCTGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC
  cadececerdeceacaerdaderregerecracadadadadaderecreeredrecearee
  reasaccerasaccerassacrassacrascerassacrassacrassacrassacrassacac
  TACACCTGCCGAGCGGAGACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG
   GTCACACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC
   CCCTCCCAGCCCTCAGACCCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGAA
  AAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGGAATCGGCATCACGGCT
   GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC
   <u> TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGGATTCAGGGCGC</u>
  AACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT
  938
   1058
  1118
  1178
  1027
   1238
   1298
  1147
  1358
   1207
  1418
   1267
  1478
   1327
  1538
  1387
  1447
  1658
   1507
  1718
   1567
   1598
  1778
  1627
   607
  818
   667
  878
   727
  787
   966
  847
  907
   196
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|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 998   TACACCTGCCGAGCGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG   1057     847   CAGTATCCTCCAGAGAACCTGGCTTCCCAGCAGCAACCAGCACACCTCTCTGTA   1058     1058   CAGTATCCTCCAGAGAACCTGAGATTTCCCAAGCAACAGACAG                                                                                                                                                                 | 1147 TCCGTGCACTACTCCCGGAGGCTCCTCCTGCTCCTGGGAGGCTGAGGGTCTG                          | 1658 AAGGGCTCATCTCCAGGGGGGTTTTTGGGGATTCGGGGATTGTTTTTTTT                                                                                         | 1747 TATCAGTIGCCCAGTITCCCAGAACCCAAATCATCCACTCAGGCCCCAGAATCCCAGGAG 1806 1958 TATCAGTIGCCCAGTITCCCAGAACCCAAATCACTCACTCAAGCCCCAGAATCCCAGGAG 1806 1958 TATCAGTIGCCAGATTTCCCAGAATCATCACTCACTCAAGCCCAGAAGC 2017 1807 AGCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 1866 2018 AGCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 2077 1867 GCCCGGATGCCCAAGAGCACCCAGGCGGATTATGCAAAGTTCCAA 1917 2078 GCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAAAGTTCCAA 1917 2078 GCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAAAGTTCCAA 2128 |
| 8 6 8 6 8 6 8 6 8                                                                                                                                                                                                                                                                                                                                                       | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                            | 8 6 8 6 8 6 8 6 8                                                                                                                               | 8 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|                                                                                                                                                                                                                                                                                                                                                                         |                                                                                    |                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Sequence 2176 BP; 456 A; 709 C; 604 G; 407 T; 0 U; 0 Other;  sry Match structurers and similarity al.6%; Bred. No. 0; structurers are 1729.8; DB 12; Length 2176; structurers are 1915; Conservative 0; Mismatches 2; Indels 174; Gaps 1; structurers are 1915; Conservative 0; Mismatches 2; Indels 174; Gaps 1; and TCTACTGCCACTGCTCCTCCTCGCTGGCGGCGGCCCAGGCTATGGATGG | GCCCTGACTCTGTGTTTTTTCCCGAGGCCGTTCTTGTGCCCCCCGCCAGGGGACCGAGGGGACCCGCCGAGGGGACCCGCCG | ACGGGGCTCCCTCTCCCAAGGAACCAAACCACGCCTCCCCCTTCTCAGTGCTC  ACCTTCACGCCCAGACCCAAGCAACCAACCCTCCCCCTTCTCAGTGCTC  ACCTTCACGCCCAGACCCCAGACCACACCCCCCCCCC | ### ### ##############################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosting a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood dotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunolistcohemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein cDNA of the
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   The invention relates to an isolated nucleic molecule that is at least 55% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polymucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polymucleotide having a polymucleotide capable of having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polympetide), the recombinant vectors, host cells (for producing the polympetide), the secreted polypeptide (comprising a sequence that is at least 95% certed polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or amplicating a medical condition by administering the polymucleotide cor the polypeptide. The gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity
  New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
   Ę
   Greene
  cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; preservative; human; ss; secreted protein; gene.
   ×
   Wei
  novel secreted protein gene 5 cDNA HDPCL05 #2.
   Moore PA,
   Olsen HS,
   Claim 1; Page 382-383; 454pp; English
   PR;
  ADA27152 standard; cDNA; 2338
  28-OCT-1998; 98US-0105971P.
27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0194792P.
30-OCT-2000; 200US-00836353.
  29-OCT-2001; 2001US-00984130
   Kenny JJ,
Crocker F
   (first entry)
   Kenny
   RUBEN S M.
LIU D.
CROCKER P R.
   WPI; 2003-567103/53.
P-PSDB; ADA27153.
  NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
  GREENE J M.
   Young PE,
M, Liu D,
   US2003055231-A1.
   Homo sapiens
   20-NOV-2003
  20-MAR-2003
   Ruben SM,
   disorders
   ADA27152
  (N1JJ/) (YOUN/) (KENN/) (OLSE/) (MOOR/) (WEIY/) (WEIY/)
   (RUBE/)
(LIUD/)
(CROC/)
  (GREE/)
   ρ,
  RESULT 12
  ADA27152
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   360
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  418
   620
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  680
   740
  426
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  TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTAG
  GAGGTGGAAAATGAGGACCGGGGGCCGATTCCAGCTCACTGGGGATCCCCCCAGGGAAC
  621 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG
   AGCTTCACGCCCAGGACCCACACACACGGACCTCACCTGCCATGTGGACTTCTCC
   AGAAAGGGTGTGAGGGTACAGAGGACCGTCCGACTCCGTGTGGCCCTATGCCCCCAGAGAC
   CTIGITATCAGCATTICACGIGACACACGCCAGCCCTGGAGCCCCAGGCAAAT
  TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC
  TTCTGGATACGAGTGCAGGAGTCAGTGGTGGTGGCGGAGGGCCTGTGCATCTCTGTGCCC
  TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG
   TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCCACAAACCACCAGAGTCGA
   rrcaaagcagraacraagacaaccaagggracracrargaccacacaaaccacagagraga
  GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGGATCCCGCCAAGGGGAAC
   TECTCCTTGGTGATCAGAGGCGCGCAGATGCAGGATGAGTCACAGTACTTTCGGGTG
   681 ACGGICATCIGIGIGITITAACIGGGCCITIGAGGAAIGICCACCCCCTICITICICCIGG
  ---CAGTGCTC
   741 ACGGGGCTGCCCTCCCCAAGGAACCAAACCAACGACCTCCCACTTCTCAGTGCTC
   AGCTTCACGCCCAGGACCCAGGACCACACACGACCTCACCTGCCATGTGGACTTCTCC
  AGAAAGGGTGTGAGGCGACAGAGGACCGTCCGAGTGGCCCTATGCCCCCAGAGAC
  CTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCCAGCCCCAGGGAAAT
   Gaps
  Length 2338;
   2; Indels 174;
                      Sequence 2338 BP; 494 A; 741 C; 633 G; 439 T; 0 U; 31 Other;
  DB 9;
  Score 1729.8;
Pred. No. 0;
0; Mismatches
  Query Match
Best Local Similarity 91.6%;
Matches 1915; Conservative
invention.
  861
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  61
  261
  321
   381
  441
   501
  361
   419
  427
   801
   487
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  181
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|  | 1220 906 RESULT 13 ADD19239 1280 XX AC AC AC ADD19239; XX 1340 XX 1026 XX AC ADD19239; XX 1140 XX 1026 XX 1026 XX 1026 XX 1020 XX 1026 XX 1030 XX Human secr | KW neuroprotective; gynaecologica KW cardiovascular-Gen; nephrotrop KW cardiovascular-Gen; nephrotrop KW respiratory-Gen; nimunosuppres KW neural disorder; nimuno system CTC 1146 KW muscular disorder; reproductiv KW pulmonary disorder; reproductiv KW pulmonary disorder; reproductiv KW inflammatory disorder; prolife KW inflammatory disorder; prolife KW KW CTG 1206 KW No2003052377-A2. | 1266 XX<br>1640 XX<br>1326 XX<br>1700 PR<br>XX<br>1700 PR<br>1386 XX | 1/50<br>1446<br>1820<br>1506                                          | 1566<br>1940<br>1626<br>2000<br>1686<br>2060                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|--|--------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|  |                                                                                                                                                              | 0-0 0-0 6-6                                                                                                                                                                                                                                                                                                                                                                                       | 1207 CACTGCAGCTGCTCCCCAGGCCAGCCCGCTCTCTGCGCTGGTGGCTTGGGGGGGG         | 1387 TGTGAGGCTGGAACGTCCATGGGGCCCAGGGGTCAGCTCTGGCCTCAGCCTCAGCTCCCCCCCC | 1507 CTTCTTTCCTCTGCCTGGCCCTGATCATGAAGATTCTACCGAAGAGACGGACTCAG  [188] CTTCTTTCCTCTGCCTGGCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAG  [189] CTTCTTTTCCTCTGCCTGGCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAG  [180] ACAGAACCCCGAGGCCCAGGTTCTCCCGGCAACGATCCTGGATTACATCATGTG  [194] ACAGAACCCCGAGGCCCAGGTTCTCCCGGCAACGAACCAGGATTACATAATGTG  [182] ACAGAACCCCGAGGCCCAGGTTCTCCCGGCAACGCAACACATCATGTG  [182] GTCCCGACGGCTCGCCCCTGGGTTCTCAGAAGCGGAATCAGAAAGCCACAAACAGTCCT  [183] CTCCCGACGGCTCGCCCCTGGGTTCTCAGAAGCGGAATCAGAAAGCCACCAAACAGTCCT  [183] CTCCCGACGGCTCGCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACCAAACAGTCCT |

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CTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAGCAG 1746
  CCCAGITICCCAGAACCCAAAICAICCACTCAAGCCCCAGAAICCCAGGAG 1806
   GAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 2240
  otein, cytostatic; antibacterial, virucide;
gynaecological; gastrointestinal-Gen; cardiant;
n; nephrotropic, antihiflammatory; muscular-Gen;
immunosuppressive, cerebroprotective; vasotropic;
lergic; cancer; bacterial infection; viral infection;
immune system disorder; blood disorder;
reproductive disorder; gastrointestinal disorder;
r; cardiovascular disorder; renal disorder;
rder; proliferative disorder; human; ss; gene.
  CTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAAGAACAGAAAAAGCAG
  cecaetricecaeaacecaarcarecaercaaececeaearcecaeae
   GAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG
   CCCAAGGGCACCCAGGCGGATTATGCAGAAGTCCAAGTTCCAA 1917
  CCCAAGGGCACCCAGGGGGATTATGCAGAAGTCAAGTTCCAA 2291
  creted protein gene 56.
   CDNA; 3264 BP
   t entry)
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ic acids encoding signal transduction pathway component ul for diagnosing, treating, and/or preventing cancer, infections, cardiovascular and inflammatory

66; 554pp; English.

The invention relates to an isolated nucleic acid molecule (CDNA) encoding a human secreted protein, representing one of 85 novel genes. Also included are recombinant vectors, host cells (expressing the protein), the secreted proteins (including their fragments, epitopes and diagnosing a pathological condition or susceptibility to the protein, of appropriating a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the nucleic acid and diagnosing a condition based on the presence or susceptibility to a pathological condition of comprising determining the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression

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the protein), preventing, treating or ameliorating a medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the activity. The nucleic acids and proteins display the following activities Cytostatic, antibacterial, virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen, Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen, Cardiovascular-Gen, Nephrotropic, Antiallar-Gen, Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic, Notropic, Antiallergic. The methods and compositions of the present incomposition disorders related to the novel polypeptides, such as cancer, bacterial or viral infections, and neural, immune system, blood, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, creating inflammatory or proliferative disorders (many examples of these diseases and disorders are given in the specification). The present sequence encodes a novel secreted protein of the invention.
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Sections 3264 BP: 804 A: 965 C: 849 G: 646 T: 0 U: 0 Other:

| 646 T; 0 U; 0 Other;            | , DB 10; Length 3264;<br>0;<br>nes 0; Indels 175; Gaps 2;              | CTGGGCGGGTCCCAGGCTATGGATGGGAGA 60     | CTGGGCGGGTCCCAGGCTATGGATGGGAGA 102                      | STGCCGGAGGCCTGTGCATCTCTGTGCCC 120                            | stacces - eccreteration                                      | ACAGGGTCTACCCCAGCTTATGGCTACTGG 180                        | ACAGGGTCTACCCCAGCTTATGGCTACTGG 221                        | SCTCCTGTGGCCACAACCACCAGAGTCGA 240                            | GCTCCTGTGCCACAAACCACAGAGTCGA 281                            | CAGCTCACTGGGGATCCCGCCAAGGGGAAC 300                           | CAGCTCACTGGGGATCCCGCCAAGGGGAAC 341                          | CAGGATGAGTCACAGTACTTCTTTCGGGTG 360                           | CAGGATGAGTCACAGTACTTTTCGGGTG 401                            | ATGAACGATGGGTTCTTTCTAAAAGTAA 418               | ALGAACGALGGGTICTITCTAAAAGTAACA 461              | 418 | CCCGAGACCCTGGAGCCCGGGAGCGGTG 521                             | 418 | GAGGAATGTCCACCCCTTCTTTCTCCTGG 581                       |     | AAACCAACGACCTCCCACTTCTCAGTGCTC 641                       | ACCGACCTCACCTGCCATGTGGACTTCTCC 486                      | ACCGACCTCACCTGCCATGTGGACTTCTCC 701 | CGACTCCGTGTGGCCTATGCCCCAGAGAC 546                             | caacrecararacceccaaaaac 761     |
|---------------------------------|------------------------------------------------------------------------|---------------------------------------|---------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------|-----------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------|-------------------------------------------------|-----|--------------------------------------------------------------|-----|---------------------------------------------------------|-----|----------------------------------------------------------|---------------------------------------------------------|------------------------------------|---------------------------------------------------------------|---------------------------------|
| 3264 BP; 804 A; 965 C; 849 G; 6 | tch al Similarity 91.6%; Pred. No. 0; 1916; Conservative 0; Mismatches | ATGCTACTGCCACTGCTGCTCCTCGCTGCTGGCGGGT | ATGCTACTGCCACTGCTGCTGCTCGCTGCTGCGCGGGCTCCCAGGCTATGGATGG | TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC | TICTEGATACGAGTGCAGGAGTCAGTGATGGTGCCGGA-GGCCTGTGCATCTCTGTGCCC | TGCTCTTTCTCCTACCCCGACAAGACTGGGACGACCTACCCCAGCTTATGGCTACGG | TECTITICICCTACCCCGACAAGACTGGACAGGTCTACCCCAGCTTATGGCTACTGG | TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACGAGAGTCGA | TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAACCACCAGAGTCGA | GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGAATCCCGCCAAGGGAAC | GAGGTGGAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAA | TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG | TGCTCCTTGGTGATCAGAGGCGCGAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG | GAGAGGAAGCTATGTGAGATATATTCATGAACGATGGGTTCTTTCT | GAGAGGAAGCTATGTGAGATATATTTCATGAACGATGGGTTCTTTCT |     | GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG |     | ACGGTCATCTGTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTTCT |     | ACGGGGGCTGCCCTCCCCAAGGAACCAAACCAACGACGTCCCACTTCTCAGTGCTC | AGCITCACGCCGGGACCCCAGGACCACACACGCCACCTGCCATGTGGACTTCTCC | AGCTTCACGCCCAGACCCCAGGACCACACACA   | AGAAAGGGTGTGAGGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC | AGAAAGGGTGTGAGCGCACAGAGGACCGTCC |
| Sequence                        | Query Match<br>Best Local S:<br>Matches 1916                           | 1 7                                   | 43 7                                                    | 61.3                                                         | 103                                                          | 121                                                       | 162                                                       | 181                                                          | 222                                                         | 241 (                                                        | 282                                                         | 301                                                          | 342                                                         | 361 (                                          | 402                                             | 419 | 462                                                          | 419 | 522                                                     | 419 | 585                                                      | 427                                                     | 642                                | 487                                                           | 702                             |
| SO                              | õμχ                                                                    | ò                                     | qq                                                      | ò                                                            | QQ                                                           | ò                                                         | QQ                                                        | δ                                                            | qq                                                          | 8                                                            | QQ                                                          | ò                                                            | qq                                                          | ò                                              | qq                                              | à   | qq                                                           | ò   | g                                                       | ò   | qq                                                       | ò                                                       | СP                                 | à                                                             | g                               |

| ò       | CITGITAICAGCAITICACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | H-1           |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|
| QQ<br>O | 2 CTTGTTATCAGCATTTCACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AT 82         |
| ð í     | 07 GTCCCATACCTGGAAGCCCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ც <u>—</u> ც  |
| 9       | Greccataceregaageeera                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 90            |
| ે દે    | 67 CAGCCCCTGCCACACTGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | CCATCC 726    |
| g (     | 82 CAGCCCCTGCCACACIGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | , ,           |
| රු ස්   | 727 TGGGGCCCTAGACCCTGGGGCTGCCGGGGGTGCCGGGGGTAAGGCTGGGGGATTC  727 TGGGGCCCTAGACCCTGGGGCTGGAGGTGCCGGGGGTTAAGGCTTGCGGGATTC  727 TGGGGGCCCTAGAGACCTGGGGGGTGGCGGGGGGGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | AGGCGC /86    |
| 3 8     | 4Z TACACCCIRCACCCCCICCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TG 84         |
| 2 A     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | -<br> -<br> - |
| δ       | ATCCTCCAGAGAACCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 9 AA 9        |
| Ор      | 2 CAGTATCCTCCAGAGAACCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AA 11         |
| δ,      | 7 AACCTTGGGAACGGCACGTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | .GT 96        |
| Db      | 22 AACCTTGGGAACGGCACGTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | GT 11         |
| δλ      | 67 GTCACACAGCAGCCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | )<br> -<br> - |
| Db      | 82 GTCACACACAGCCCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ,ĠĊ 12        |
| ζŏ      | 27 CCCTCCCAGCCCTCAGACCCCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CGAA 10       |
| Op      | 2 decreedadecreadadeced                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | CGAA 13       |
| ,<br>,  | 1087 GGAGAGTICACCIGCCACGCCCCACIGGCTCCCAGCACGTCTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | CAGCCTC 1146  |
| Db      | 02 GGAGAGTTCACCTGCCACGCTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ccrc 13       |
| ζ       | 1147 TCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCTG 12       |
| QD      | 62 TCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTTCCTGCTCCTGGAGGCTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCTG 1        |
| ò       | 07 CACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTGTGCGGCGGTGGTGGTGGTGGTTGTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | GGAG 126      |
| qq      | 22 cactecadotrocrecimentes de consecuencia de | GGAG 148      |
| ζ       | 67 GAGCTGCTGGAGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | CGGG 132      |
| QQ      | 82 GAGCTGCTGGAGGGGAACAGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ceee 15       |
| ò       | 27 CCCTGGGCCAACAGCTCCCTGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCGC 138      |
| qq      | <u>ccreeccadadecreectecteragegereagegereagerecgeeere</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | GGGG 160      |
| δ       | 7 TGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TAAG 144      |
| Dp      | ĠŦĠĀĠĠĊĊŦĠĠĀĀĊĠŦĊĊĀŦĠĠĠĠĊĊĊĀĠĀĠŦĠĠĀŦĊĊĀŦĊĊ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | AGATAAG 1661  |
| ά       | 7 AAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | CACGGCT 150   |
| ΩÞ      | 62 AAGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | caceer 1721   |
| ٥٧      | CITITICCICGCCGGCCCGAICAIGAAGAITCIACCGAAGAGAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | GACTCAG 1     |
| ΩÞ      | TTCTTTTCCTCTGCCTGGCCCTGATCATCATGAGATTCTACCGAAGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | GACT          |
| ζ       | SAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | CAATGTG 1     |
| ΩÞ      | CAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | AAT           |

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1687 CGGACCCCTCTTCCACCAGGTGCTCCCCCAGAATCAAAGAAGAACAGAAAAAAGAG 1746
  1747 TATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAG 1806
   1962 TATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAG 2021
  1807 AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 1866
  2022 AGCCAAGAAGAACTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG 2081
  1902 GGGACCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAAAAGCAG 1961
   1867 GCCCGGATGCCCAAGGCCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917
   2082 GCCCGGATGCCCAAGGCACCCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 2132
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ABK43362 standard; cDNA; 2823 BP ABK43362;

(first entry) 05-JUN-2002

DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3c.

Human; sialic acid-binding Ig-related lectin; SIGLEC, asthma; mamune system disease; leuksemia, allergy; inflammatory disease; tissue damage; allergic thinitis; ostecarthritis; Crohu's disease; psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.

Homo sapiens

WO200208257-A2.

31-JAN-2002.

20-JUL-2001; 2001WO-US023082.

21-JUL-2000; 2000US-0220139P.

(BRIM ) BRISTOL-MYERS SQUIBB

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Whitney G;

Longphre M, Chang H,

WPI; 2002-241565/29. P-PSDB; AAU87076.

Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

Claim 11; Fig 4A; 209pp; English.

The invention relates to an isolated SIGLEC (stalic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow-up assays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleoide sequences and/or SIGLEC-BMS and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS ABSOLT 14
ABSCA3362
ABSCA3

1318 1077

TJGGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCT

1259

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P-PSDB; AAU87074.

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   1618
   TCACGGCTCTTCTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGA 1558
   GGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACA 1437
   TCAATGTGGTCCCGACGGCTGGCCCCTCAGAAGCGGAATCAGAAAGCCACACAA 1678
   TCAATGTGGTCCGGACGGCTGGCCCCCTCAGAAGCGGAATCAGAAAGCCACACAA 1497
   ACAGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGA 1738
   ACAGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGA 1557
   AAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAAT 1798
   CCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCA 1858
  CCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCA 1677
TTGGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCT 1137
  GECCTGAGGCCCGGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAAGTTCAA 1736
  GGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917
  CAGATAAGAAGGGACTCATCTCAACGGCATTCTCCCAACGGAGCGTTTCTGGGAATCGGCA
  TCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGAC
   GGACTCAGACAGAAACCCCCGAGGCCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACA
                            CAGCCGGCCCTGGCCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCA
  cadecedeceredecedacaderecereadecerecardeadedereaderecedeceda
   CAGATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGGGTTTCTGGGAATCGGCA
   encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3a
   Human, sialic acid-binding Ig-related lectin, SIGLEC, asthma; mimune system disease, leukaemia, allergy; inflammatory disease, tissue damage, allergic rhinitis; osteoarthritis, Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis; gene, ss.
  Ö
  ABK43360 standard; cDNA; 2565 BP
   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  2000US-0220139P.
   20-JUL-2001; 2001WO-US023082
  (first entry)
   Chang H,
  WPI; 2002-241565/29
   WO200208257-A2
   21-JUL-2000;
  Homo sapiens
   Longphre M,
  31-JAN-2002,
  05-JUN-2002
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such a sathmain, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, following asserts, psoriases such as allergic rinitis, or drugs which inflammatory diseases such as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity or SigLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SigLEC-BMS nucleotide sequences and/or SigLEC-BMS care useful as mucleic acid probes are useful for screening genomic library to isolate a genomic clone of SigLEC-BMS antibodies are also useful as mucleic acid probes of sigLEC-BMS suithodies are also useful as mucleic calls expressing SigLEC-BMS proteins and in diagnostic imaging technology.

The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SigLEC-BMS proteins and in diagnostic imaging technology.
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  360
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   420
   548
  480
  608
  540
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  Novel isolated SIGLEC (stalic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
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   TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC
   TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG
  TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGCTATGGCTAGG
  TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA
   TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA
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  GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
  TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGAGTACTTCTTTCGGGTG
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  GTGCTCAGCTTCACGCCCAGACCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC
   TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCCTATGCCCCC
   285;
  Length 2565;
  Sequence 2565 BP; 627 A; 765 C; 656 G; 517 T; 0 U; 0 Other;
   Indels
   69.7%; Score 1337; DB 6;
Larity 85.1%; Pred. No. 3.1e-308;
Conservative 0; Mismatches 0;
   11; Fig 2A; 209pp; English
  ATGCTACTGCCACTGCT
  Best Local Similarity
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| Oy 1861 CCTGAGGCCCGGATGCCCAAGGCACCCAGGCGGATTATGCAGAAGTTCAA 1917    | 1861<br>1704<br>h complet<br>ime : 133 |
|--------------------------------------------------------------------|----------------------------------------|
|                                                                    | 186                                    |
|                                                                    | 1644                                   |
| 01 CAGGAGGCCAAGAGGACTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1860 | 1801                                   |
| AAGCAGTATCAGTTGCCCAGTTTCCCAGA                                      | 1584                                   |
| 41 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACGCCCAGGAATCC 1800   | 1741                                   |
|                                                                    | 1524                                   |
| 31 AGTCCTCGGACCCCTCTTCCACCAGGGCTCCCTCCCCAGAATCAAAGAAGAACAGAAA 1740 | 1681                                   |
|                                                                    | 146                                    |

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9 08:30:01 2004
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November 5, 2004, 13:50:18; Search time 112.542 Seconds (without alignments) 2617.614 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
  OM protein - protein search, using sw model
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| Title:  |        | US-09-937-636-3 |
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1 MLLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 512 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1825181 seqs, 575374646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|           | Ω<br>O        | Q961c7 homo sapien | homo s | 3 homo | 3 hon    | homo sa    | พนธ ก  | mus ก  | Q7z728 homo sapien | homo       | homo       | pan t      | mus m  | 14 mu    | Aag72479 mus muscu |          | Q91y57 mus musculu | homo       | homod  | homo       |            | рошо       | 16 hon   | homod  | 5 home | 9 homo | 19 hor | homo sa    | mus r      | Q8btg2 mus musculu | . Q80ze2 mus musculu | Q8iw38 homo sapien |
|-----------|---------------|--------------------|--------|--------|----------|------------|--------|--------|--------------------|------------|------------|------------|--------|----------|--------------------|----------|--------------------|------------|--------|------------|------------|------------|----------|--------|--------|--------|--------|------------|------------|--------------------|----------------------|--------------------|
| SUMMAKIES |               | SILA HUMAN         | Q6UXI8 | $\sim$ | BAC85493 | SILB HUMAN | Q80ZE3 | Q8BY18 | 072728             | SIL8 HUMAN | SILL_HUMAN | SILL PANTR | Q6PJ50 | AAQ79834 | AAQ72479           | AAH23280 | SIL5 MOUSE         | SIL9 HUMAN | Q6GTU4 | SIL6_HUMAN | SIL7 HUMAN | SIL5 HUMAN | AAH29896 | Qeuxgo | 373    | 10     |        | CD33 HUMAN | SILF MOUSE | ū                  | Q80ZE2               | Q8IW38             |
|           |               | 7                  | ゼ      | 4.     | 'n       | v          | œ      | m      | 499 2              | n          | S.         | 7          | 80     | œ        | 00                 | œ        | 7                  | m          | 6      | N          | 7          | _          | ы        | 4      | 4      | 7      | 4      | 4          | σ          | 6                  | ო                    | 4                  |
| о¥        | $^{rY}_{ch}$  | 5.                 | 83.7   | 'n     | ٥.       | ů.         |        | •      | 35.3               | 'n.        | m.         | 'n         | ď.     | å        | ٠                  | ď.       | ς.                 | ď          | ÷      | ö          | 30.8       | φ.         | φ.       | ٠      | 6      | 9      | 'n     | 'n.        | 25.5       | 4.                 | m.                   | 9.                 |
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| Aas89010 pan trogl<br>Aas89009 pan panis                                                              | Aas89008 gorilla g<br>Aas89011 homo sapi | Q8bu57 mus musculu<br>Bac27845 mus muscu |                    | Q95kp9 gorilla gor<br>Q95kq0 pan paniscu | Q95kp8 pongo pygma<br>P20916 homo sapien | Q92154 coturnix co |
|-------------------------------------------------------------------------------------------------------|------------------------------------------|------------------------------------------|--------------------|------------------------------------------|------------------------------------------|--------------------|
| AAS89010<br>AAS89009                                                                                  | AAS89008<br>AAS89011                     | Q8BU57<br>BAC27845                       | Q9P0F8<br>AAO26206 | Q95KP9<br>Q95KQ0                         | Q95KP8<br>MAG HUMAN                      | SMP_COTJA          |
| 00                                                                                                    | 100                                      | 04 04                                    | ~ ~                | 0 0                                      | 7                                        | н                  |
| 233                                                                                                   | 233<br>233<br>333<br>333                 | 423<br>293                               | 287                | 269                                      | 269<br>626                               | 620                |
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| 122<br>122<br>123<br>134<br>135<br>136<br>136<br>136<br>136<br>136<br>136<br>136<br>136<br>136<br>136 | 525<br>515<br>14                         | 471.5                                    | 371.5<br>362.5     | 360.5                                    | 351.5                                    | 302.5              |
| 332                                                                                                   | 3 3 4<br>6 53 4                          | 37                                       | 3<br>9<br>4<br>0   | 4 4<br>1 2                               | 4 4<br>6 4                               | 45                 |

## ALIGNMENTS

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Etapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Militip M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Asalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Sc
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masked by cis interactions with sialic acids on the same ceîl surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatases(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
dependent binding to cells. Preferentially binds to alpha2.3- or
2,6-linked sialic acid. The sialic acid recognition site may be molecules.

SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4); secreted (isoform 5).
ALTERNATIVE PRODUCTS: SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation. Event=Alternative splicing; Named isoforms=5;

IsoId=Q96LC7-2; Sequence=VSP\_002565; Name=3; Synonyms=Sv3; IsoId=Q96LC7-3; Sequence=VSP\_002564; IsoId=Q96LC7-1; Sequence=Displayed; Name=2, Synonyms=Short, Sv1

Name=4; Synonyms=Sv4;
IsoId=096LC7-4; Sequence=VSP\_002561;
Name=5; Synonyms=Sv2;
Name=5; Synonyms=Sv2;
IsoId=096LC7-5; Sequence=VSP\_002562, VSP\_002563;
TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
feosinophils, monocytes and a natural killer cell subpopulation).
Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal

chord. Isoform 2 is also found in brain. Isoform 4 is specifically bound in natural killer cells.

DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation --!- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.

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or send an email to license@isb-sib.ch)
                            EMBL; AY029277; AAK40255.1; -.
   EMBL;
EMBL;
HSSP;
  EMBL;
  EMBL;
   EMBL;
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181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240

ò

| Signal;                                                                       | e lectin 10.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | (Potential). 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| sion; Glycoprotein;<br>Phosphorylation; Repeat;                               | * .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Allarity.  Harity.  Harity.  Harity.  Harity.  Harity.  Glounc) (Poed (Glounc)                                                                                                                                                                                                                                                                                                                                              | TALTQKPDVVIPETLEPGGPVTVICVY TALLAL-> TGRRWGGNPCLSHWGGT LOHKNLPPRSLSQP (in lsoform) /FTId=VSP 002662.  Missing (in lsoform 5). /FTId=VSP 002663.  Missing (in lsoform 3). /FTId=VSP 002663.  Missing (in lsoform 2). /FTId=VSP 002665.  Missing (in lsoform 2). /FTId=VSP 002665.  Missing (in lsoform 2). /FTIG=VSP 002665.  Y->F: Abolishes binding to S-> P: (in Ref. 4). P-> S (in Ref. 4). P-> S (in Ref. 3). | 1; beng 7; 1 inde1 Svpcsfsyp Svpcsfs |
| LECIO.  g-like.  g_c2.  g_MHC.  2.  1rke; 3.  HC; 1.  Cell adhe Lectin;       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 7,7,0<br>0,7,0<br>0,0<br>0,0<br>0,0<br>0,0<br>0,0<br>0,0<br>0,0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 85<br>99<br>99<br>99<br>99<br>99<br>99<br>90<br>90<br>90<br>90                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | imilarity 73.0%; Score 2576.5; DB Conservative 1; Mismatches MLDFLLESSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCI MLSTAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPA FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPA FRGSYVRYNFWNDGFFLKVTALTQKEDVYIPETLEBG ERGSYVRYNFWNDGFFLKVTALTQKRDDVIPETLEBG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 5620;<br>007110<br>003598<br>003006;<br>ig;<br>ig;<br>1Gc<br>8; IGc<br>835; I | SIGNAL  SIGNAL  11 ( CHAIN  17 ( CHAIN  17 ( CHAIN  17 ( CHAIN  18 ( CHAIN  19 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 140<br>186<br>141<br>445<br>667<br>28<br>134<br>226<br>324<br>440<br>625<br>697 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ch 1 Si 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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   303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE, 362
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  423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPPGAPSKK 482
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  FKAVTETTKGAPVATNHQSREVEMSTRGR FQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
   183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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   1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd Eaton J., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
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Primata; Catarrhini; Hominidae;
   Created)
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Last annotation update)
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74.8%; Pred. No. 4.8e-146;
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   121 ERGSYVTYNFMNDGFFLKVT----
   (TrEMBLrel. 27, (TrEMBLrel. 27, I
  Query Match
Best Local Similarity 74.8
Matches 450; Conservative
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Eukaryota, Metazoa, (
Mammalia, Eutheria, 1
   NCBI_TaxID=9606;
  FQ 512
   FO 544
   AAQ88703;
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                      NCBI_TaxID=9606;
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SILB HUMAN
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  NOKKQYQLPSPPPEPKSSTQAPESQESQESLHYATLNPPGVRPRPEARMPKGTQADYAEVK 542
  ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
  183 LVISÍSRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242
  -----PPENLRVMVSQANRTVLE 270
   243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
  271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330
   362
  NOKKOYOLPSFPEPKSSTOAPESOESOELHYATLNFPGVRPRPEARMPKGTOADYAEVK 510
   GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422
   9
   OZ-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
CDNA FLJ16031 fis, clone SPLBNZ001599, weakly similar to Homo sapiens
sialic acid binding immunoglobulin-like lectin 8 long splice variant
(Siglec8) gene.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
  181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
   -------VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
   GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
  KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
  1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAYGYW
  PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
   61 FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
   1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
  121 ERGSYVTYNFMINDGFFLKVT------
  Indels 148; Gaps
Dewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi.S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Fifter to Identify Novel Human Secreted and Transmembrane Proteins: Disconformatics Assessment."

Bioinformatics Assessment."

Bioinformatics Assessment."

Biolifer to Gentley A., AAGEREA AAGEREA A., AAGEREA AAGEREA A., AAGER
   Length 544;
  Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Sc. Schadgiri S., Simmons L., Singh J., Smith V., Stinson Adatanabe C., Wieand D., Woods K., Xie M.H. V. Yuan J., Zhang M., Zhang Z., Goddard A. Godowski P.;

Right The Secreted Protein Discovery Initiative (SPDI), a virial Effort to Identify Novel Human Secreted and Transmemb Bioinformatics Assessment.";

Right Genome Res. 13.2265-2270(203).

Right Genome Res. 13.2265-2270(203).

Right Ays S8337; AAQ88703.1; -.

SCOVE 2265; DB Z; Leng Best Local Similarity 74.8%; Pred. No. 4.8e-146; Leng Best Local Similarity 74.8%; Pred. No. 4.8e-146; Leng Matches 450; Conservative I; Mismatches 3; Inc
   425 AA
   241 LVISISRDNTPD----
   PRELIMINARY;
  FQ 512
  G.
   BAC85493
BAC85493;
  511
   121
  141
  331
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  391
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KNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPPBARMPKGTQADYAEV 509
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  ENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEH
  EGEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKIL
  303 PKRRIQIETPRPRESRHSTILDVINVVPTAGPLVQKRNQKATPSSPRTPLPPGAPSPESK
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  1 MVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGR
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   210 DTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVL
   BGEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKIL
   PKRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESK
  90 FQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVY
   61 POLTGDPAKGNCSLVIRDAQMQDESQYFPRVERGSYVRYNFMNDGFFLKVT-----
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic acid-binding lectin 11) (UNQ5222/PRO28718).
Homo sapiens (Human).
  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Mabo Inman CDNA sequencing project.";
"NEDO Inman CDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
   80.7%; Score 2185; DB 2; Length 425; 87.2%; Pred. No. 1e-140; tive 2; Indels 58
Eutheria; Primata; Catarrhini; Hominidae; Homo.
  425 AA; 47345 MW; 809854127B397D73 CRC64;
   686 AA
  EMBL; AK122619; BAC85493.1; -.
  Query Match 80.7
Best Local Similarity 87.2
Matches 421; Conservative
   STANDARD;
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329

182

149 111

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209 122 389

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362

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241 LVISISRDNTPD-----
  74544 MW;
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  Matches 323; Conservative
   84
353 3
686 AA;
  Similarity
  Transmembrane.
   CHAIN
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DISULFID
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   122
   182
  CARBOHYD
VARSPLIC
   181
   253
  333
  Query Match
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REQUENCE FROM N.A. (ISOFORM 2).

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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Isoid=Q96RL6-2; Sequence=VSP_008764; ISSUE SPECIFICITY: Expressed by macrophages in various tissues including Kupffer cells. Also found in brain microglia. DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the imminoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                     SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PTPN6 AND PTPN11. MEDLINE=22086217; PubMed=11986327; DOI=10.1074/jbc.M202833200; Angata T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R.,
  essed by
  "Cloning and characterization of human Siglec-11. A recently evolv
signaling that can interact with SHP-1 and SHP-2 and is expressed
tissue macrophages, including brain microglia.";
J. Biol. Chem. 277:24466-24474 (2002).
   Containing phosphatases.

PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-limite lectin) family.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
  Event=Alternative splicing; Named isoforms=2;
  Isold=Q96RL6-1; Sequence=Displayed;
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  InterPro, IPR007110; Ig-like InterPro, IPR003006; Ig_MHC.
  HGNC:15622; SIGLEC11.
   HSSP; Q9Y286; 107S.
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Pfam; PF00047; ig; 3. TPROSITE; PS50835; IG\_LIKE; 3.

MIM; 607157;

Genew;

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TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
   181
  421
   FKGRISPKIGAPVAINNOSREVEMSTRDRFQLIGDPGKGSCSLVIRDAQREDBAWYFFRV 121
  |:|||| |||
242 LIISISHDNTSALELQGNVIYLEVQKGQFIRRLLCAADSQPPATLSWVLQDRVLSSSHPWG 301
   302 PRTLGLELRGVRAGDSGRYTCRAENRLGSQQQALDLSVQYPPENLRVMVSQANRTVLENL 361
   9
   61
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  1 MILIPILLSSLIGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
  FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
   ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
   482 LEGNSSQGSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCKAWNVHGAQSGSVFQLLPGKL
  Gaps
   Potential.
Sialic acid binding Ig-like lectin
Extracellular (Potential).
  (Potential). (Potential). (Potential). (Potential).
  (Potential).
(Potential).
(Potential).
  VHGAQSGSVFQLLPG -> W (in isoform 2)
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Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
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  Potential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 3.
ITIM motif.
   By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N'linked (GLONAC. ...) (EN Inneed (GLONAC. ...) (EN INNE
   E -> A (in Ref. 2)
A -> G (in Ref. 2)
   /FTId=VSP
   ò
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| Db 299 RTLALELEWVKAGDSGHYTCQAENRIGSQQHTLDLSVLYPPQDLRVTVSQANRTVEHLRR  Qy 274 NGTSLPVLEGQSLCLVCVTHSSPBARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF  Db 339 NAISLPVLEGQSLCLVCVTYSNPPANVSWAWVTQTLIPIQSSEPGVLELPLVQREHEGEF  Qy 334 TCHARHPLGSQHVSLSLSVHYKKGL | OY 361 TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVUPTAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | PRT;<br>eate<br>st a<br>st a<br>ymus<br>uct:<br>Cran<br>Sciu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                           |
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|                                                                                                                                                                                                                                                 | RESULT 6 2802E3 (#D) QROZE3 (#D) QROZE3; (#D) QROZE3; (#D) QROZE3; (#D) O1-UTN-2003 (TrEMBLrel. 24, Created) (DT 01-UTN-2004 (TrEMBLrel. 26, Last sequence update) (#D) O1-MAR-2004 (TrEMBLrel. 26, Last annotation update) (#D) Name=Siglec10; (#N) Name=Siglec10; (#N) Name=Siglec10; (#N) Name=Siglec10; (#N) Name=Siglec10; (#N) Mus musculus (Mouse). (#N) Musculus (Musculus (Musculus Musculus (Musculus (Musculu | IBL_TRAXID=10090;  SQUENCE FROM N.A.  FRAIN=ALB/C;  STAIN=ALB/C;  STAIN=ALB/C;  TAMAN=ALB/C;  TAMAN= | Query Match Query Match Query Match Best Local Similarity 43.0%; Score 1343.5; DB 2; Length 088;  Best Local Similarity 43.0%; Pacci, No. 4.2e-83;  Query Conservative 67; Mismatches 138; Indels 189; Gaps 10;  2 LLPLISSLIGGSQANDGRFMIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAXGYWF 61  3 LLLFLISFLLDGPQGQMESYFLQVQRIVKAQEGLCIFVPCSFSSPEGKWLNRSPLYGYWF 62  Query 62 KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121  pb 63 KGIRKFSLSFPVATNNKDKVEWMEARGRFQLLGDISKKNCSLLIKDVQWGDSTNYFFRME 122 | DD   122 RGSYVRYNFWNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAFEBCPPPBFSWT 181 |

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sequences.";
nd. Sci. U.S.A. 99:16899-16903(2002).
   Created)
Last sequence update)
Last annotation update)
  421 PLACKRNOKATPNSPRTPLP 440
  599 SLA--RNWKAEPDAPSRSSP 616
   EMBL; BC053319; AAH53319.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
   SMART; SM00408; ĪGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Hypothetical protein.
   01-0CT-2003 (TrEMBLrel. 25, 101-0CT-2003 (TrEMBLrel. 25, 101-MAR-2004 (TrEMBLrel. 26, 14) Pypothetical protein. Homo sapiens (Human).
   Query Match
Best Local Similarity 42.3
Matches 224; Conservative
   Pfam; PF00047; ig;
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   Proc. Natl. Acad.
   NCBI_TaxID=9606;
  mouse cDNA
  rissum=Spleen;
   359
  361
  SECUENCE
   Q7Z728
  RESULT 8
Q7Z728
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   STRAIN-CS-BL/67, TISSUE-Thymus;
A dachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rudaa S., Furuno M., Hangagki T., Hara A., Hashizume W., Hayashida K., Hayatuu W., Hiracka T., Hirozane T., Hayashida K., Hayatuu M., Hirachoto K., Hiracka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Koya S., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito H., Sakai C., Sakai K., Sakatu M., Sano H., A sasaki D., Sihbata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yakuilshi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R HSSP: Q9Y286; 1075.
  252
   RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT 181
   241
   239 AIŚIFHDNVSVPDLHENPSHLEVQQGQSLRLLCTADSQPPATLSWVLEDQVLSWSSPVGS 298
  274 NGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF 333
   62 KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121
  -----PPENLRVMVSQANRTVLBNLG 273
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   61
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STRIN=C7JEL/6J, TISSUE=Thymus,

STRIN=C7JEL/6J, TISSUE=THYMUS,

MEDLINE=20530913, PubMed=11076861;

A Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

A Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

A Namamoto H., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K.,

A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa Y., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Ishikawa M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
   299 RILALELPWVKAGDSGHYTCQAENRLGSQQHTLDLSVLYPPQDLRVTVSQANRTVLEILR
  2 LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF
   LILFILISFILDGPQGQMESYFLQVQRIVKAQEGLCIFVPCSFSSPEGKWLNRSPLYGYWF
   182 GAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL
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   ; Score 1211.5; DB 2; Length 623;
; Pred. No. 3.7e-74;
55; Mismatches 111; Indels 187;
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GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR00710; Ig-like.
InterPro; IPR003598; Ig_c2.
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SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
  44.88;
43.18;
   Query Match
Best Local Similarity 43.1%
Matches 267; Conservative
  623 AA;
   SEQUENCE FROM N.A.
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13;
   MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Ratusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Ratusberg R.L., Feingold E.A., Grouse L.H., Schaefer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Astapletcon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.E., Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A., Muting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Arthing M.I., Colmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
   TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAG 420
359 NAISLPVLEGQSLCLVCVTYSNPPANVSWAWVTQTLIPIQSSEPGVLELPLVQREHEGEF 418
   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
   479 EGNSSNASFTVTFSSLGPWVNSSLSLLQELGPSLWLSCESWNTHGAQTTSVLLLPDKDSA
  Gaps
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  16;
  Length 499;
  35.3%; Score 955; DB 2; Length 49
42.3%; Pred. No. 8.4e-57;
ive 70; Mismatches 160; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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  349
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   283 CAVNSNPPARLSWIRGSLILCPSRSSNPGLLELPRVHVRDEGEFICRAQNAQGSQHISLS 342
  435
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                              54
   TISSUE=Eosinophil;
MEDLINE=20092847; PubMed=10625619;
Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.,
Crocker P.R.;
   1 MILLILIEPLEMETKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
   115 OYFFRVERGSY-----VRYNFMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWA
  -----PPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLV
  290 CVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS
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  170 FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
  VRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV
   405 RHSTILDYINVV---PTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSF
  Poussias G., Yousef G.M., Diamandis E.P.;
"Modecular characterization of a siglec8 variant containing
cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
Biochem. Biophys. Res. Commun. 278:775-781(2000).
   SEQUENCE FROM N.A. (ISOFORM 3).

KIKLY K.K., Bochner B.S., Ferman S.D., Tan K.B., Gallagher K.T.,

KIKLY K.K., Bochner B.S., Abrahamson J.A., Erickson-Miller C.L.,

D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,

Murdock P.R., Tachimoto H., Schleimer R.P., White J.R.;

"Identification of SAF-2, a novel siglec expressed on eosinophils,

mast cells, and basophils.",

J. Allergy Clin. Immunol. 105:1093-1100(2000).
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
  398 VGDTGMEDAKAIRGSASQGPLTESWKD----GNPLKKPPPAV-------
   PEPKSSTQAPESQESQEELHYATLNFPGVRPR-PEARMPKGTQADYAEVK 510
  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20549027; PubMed=11095983; DOI=10.1006/bbrc.2000.3866;
   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-027-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin 8 precursor (Siglec-8)
(Sialoadhesin family member-2) (SAF-2).
  499 AA
   SEQUENCE FROM N.A. (ISOFORM 3).
  Name=SIGLEC8; Synonyms=SAF2;
Homo sapiens (Human).
  STANDARD;
   239 VRLDVSY
  NCBI_TaxID=9606;
  SILB HUMAN
   350
  343
   462
   SILB_HUMAN
  SERA SE PARENTE PRESTE EN SECHERAL SE
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   S
  Isoid-gonvz4-3; Sequence=VSP_002560;
-:- TISSUB SPECIFICITY: Expressed specifically on eosinophils.
-:- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
"Siglec-8. A novel eosinophil-specific member of the immunoglobulin
  Floyd H., Zhang J.O., Crocker P.R.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2.3-linked stalic acid. Also binds to alpha2.6-linked sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

-I-SUBCELDUTAR LOCATION: Type I membrane protein.
  Sialic acid binding Ig-like lectin 8. Extracellular (Potential).
   containing phosphatases.
--- SIMITARITY: Belongs to the immunoglobulin superfamily. SIGLEC (stalic acid binding 19-like lectin) family.
--- SIMITARITY: Contains 2 immunoglobulin-like C2-type domains.
--- SIMITARITY: Contains 1 immunoglobulin-like V-type domain.
   PROSITE; PS50835; IG_LIKE; 2.
Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
   MMM, 605639; -.
GO, GO:0016621; C:integral to membrane; TAS.
GO, GO:000529; F:sugar binding; TAS.
GO, GO:0004881; F:transmembrane receptor activity; TAS.
GO, GO:0007165; P:signal transduction; TAS.
InterPro; IRR007110; Ig-1ike.
InterPro; IPR003598; Ig_C2.
  Cytoplasmic (Potential).
19-like V-type.
19-like C2-type 1.
19-like C2-type 2.
ITIM motif.
SLAM-LIKE MOTIF.
   Event=Alternative splicing; Named isoforms=3;
   By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNA
  IsoId=Q9NYZ4-2; Sequence=VSP_002559;
  IsoId=09NYZ4-1; Sequence=Displayed;
   Potential.
   Potential.
                                       Biol. Chem. 275:861-866(2000).
  EMBL; AF287892; AAG00573.1; --
EMBL; AF223403; AAF34702.1; --
EMBL; AF195092; AAF27622.1; --
EMBL; AF310234; AAK55140.1; --
HSSP; Q97286; 1078.
  SEQUENCE FROM N.A. (ISOFORM 2)
   Name=1; Synonyms=Long;
   Pfam; PF00047; i
SMART; SM00408;
                      superfamily
   Name=3
  DISULFID
DISULFID
DISULFID
CARBOHYD
   TRANSMEM
   DISULFID
  CHAIN
DOMAIN
   DOMAIN
DOMAIN
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   SIGNAL
  DOMAIN
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(GlcNAc. . .) (Potential).

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13;
   349
  PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
  120
   169
  180
  229
  238
  289
  282
   342
   404
  461
   435
  343 LSLQNEGTGTSRPVSQVTLAAVGGAGATALAFLSFCIIFIIV-----RSCRKKSARPAAG 397
   54
  9
              N-linked (Glosson, ) (Potential).
ALTHRPDILIGGLESGHSRNLTGSVPWACKGGTPPMISWI
SASVSRPGPTARSSVLTLTRKRQDHGTSLTGQVTLDGTGTV
TTTGTVKLDVSY -> D (in isoform 2).
/FTId=VSP_002559.
  GPLTEGWINGGNPLKKPPPAVAPSSGEBGELHYATLSFHKVK
PODPGGGATDSEYSEIKHKRETAETQACLRNHNPSSKEV
RG -> VSDVGFSTPEIQPGHL (in isoform 3).
/Fild=VSP_002560.
  1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
  1 MLLLLLLLLLPLLWGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
   PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG
   115 QYFFRVERGSY-----VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA
  121 SYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNLTCSVPWA
   VRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV
   CVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS
   LSVHYKKGLISTAPSN---GAFLGIGITALLFL--CLALIIMKILPKRRTQTETPRPRFS
  FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
   VRLDVSY------PPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLV
   RHSTILDYINVV---PTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSF
  Gaps
  Q96PQ1, Q81XH7;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 45, Last equence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-Li) (UNQ9215/PRO34042).
Name=SIGLECL1; Synoryms=SLG;
   Euteleostomi;
   16;
   462 PEPKSSTOAPESOESOEELHYATLNFPGVRPR-PEARMPKGTOADYAEVK 510
  SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
TISSUE=Bone marrow;
MEDLINES=21303046; PubMed=11409877; DOI=10.1006/bbrc.2001.5052;
Foussias G., Taylor S.M., Yousef G.M., Tropak M.B., Ordon M.H.,
Diamandis E.P.;
  Length 499;
  , Metazoa, Chordata, Craniata, Vertebrata, Eutele
Eutheria, Primates, Catarrhini, Hominidae, Homo
  35.0%; Score 947; DB 1; Length 49 42.1%; Pred. No. 2.9e-56; ive 70; Mismatches 161; Indels
  398 VGDTGMEDAKAIRGSASQGPLTESWKD----GNPLKKPPPAV---
  086EFF989B74123C CRC64;
(GlcNAc. : .)
  595 AA.
N-linked
   54042 MW;
   Query Match
Best Local Similarity 42.13
Matches 223; Conservative
   STANDARD;
249
245
   499
  (Human)
  Eukaryota; Metazoa;
   499 AA;
  NCBI_TaxID=9606;
249
267
152
   416
  Homo sapiens
  SILL HUMAN
  Mammalia;
  170
   290
  53
  61
  230
  405
  239
   283
   350
   VARSPLIC
   SEQUENCE
CARBOHYD
                          CARBOHYD
  VARSPLIC
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**X **X **DEALEMPS-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B., Buccow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buccow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Dequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunarathe P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; A Generation and initial analysis of more than 15,000 full-length human and mouse collabs.
  SEQUENCE FROM N.A. (ISOFORM LONG).

MEDLINE=22887256; PubMed=12975509; DOI=10.1101/gr.1293003;
A Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chin C., Crowley C., Currell B., Denel B., Dowd P., A Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Hudang A., Kim H.S., Klimcwski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Senagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vanden R., Watanabe C., Mieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., A Godowski P., Gray A.;

"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
  Name=Short; Synonyms=SiG-8; Isole-8: Specific Synonyms=SiG-8; Sequence=SNS POSS66; A specific Structure and sole of the short isoleom, it is lower expressed in spleen, small intestine and adrenal gland; it is lower expressed in thyroid, placenta, brain, stomach, bone marrow, spinal chord and beast. The long isoform is highly expressed in spleen, small intestine and bone marrow; it is lower expressed in thyroid,
   DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
  Dowd P.,
   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by dis interactions with sialic acids on the same cell
  placenta, thymus, trachea, stomach, lung, adrenal gland, fetal brain and testis.
  MEDLINES-15.539%, PubMed=11.54677; DOI=10.1074/jbc.M105926200; MADSDINES-15.539%, PubMed=11.54677; DOI=10.1074/jbc.M105926200; Angata T., Varki M. W. Varki A., Varki M. W. Varki M. W. Varki M. W., Varki M. M., Varki  containing phosphatases. SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
"Cloning and molecular characterization of two splice variants on putative member of the Siglec-3-like subgroup of Siglecs."; Biochem. Biophys. Res. Commun. 284:887-899(2001).
  SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
   Event=Alternative splicing; Named isoforms=2;
   Name=Long; Synonyms=SLG-L;
IsoId=Q96PQ1-1; Sequence=Displayed;
  SEQUENCE FROM N.A. (ISOFORM LONG)
   Genome Res. 13:2265-2270(2003).
   SSUE=Blood
   surface.
   -
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RYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALS 186
   -!- SUBGELLUIAR LOCATION: Type I membrane protein.
-!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunosceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                              XWNYIYDKLSVHVTALIHMPTFSIPGTLESGHPRNLTCSVPWACEQGTPPTITWMGASVS
  SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS
  247 RDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRG
   -----PPQNLTMTVFQGDGTASTTLRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGS
  QVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK---KGLISTAF
  418 LTLSPSQSSNLGVLELPRVHVKDEGEFTCRAQNPLGSQHISLSLSLGLNRFISGV
  364 SNGAFLGIGITALLFLCLALIIMKILPKRRIQTETPRPRFSRHSTILDYINVV---PTAG
   421 PLAQKRNQKATPNSPRTPLPP--GAPSPESKKNQKKQYQLPSFPBPKSSTQAPESQESQE
   MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200; Angata T., Varki N., Varki A.; Angata T., Varki N.M., Varki A.; Angata T., Varki N.M., Varki M.; T.; T. T. T. T. Varki N.M., Varki M.; J. Biol. Chem. 276:40282-40287(2001).

J. Biol. Chem. 276:40282-40287(2001).

-!- FUNCTION: Putathive adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell
  containing phosphatases.
-- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding 19-like lectin) family.
-- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
  Pan troglodytės (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
20-CT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Tallike lectin-like I precursor (Siglec-like molecule 1) (Siglec-Li).
   s--LDPTITRSSMLSLIPQPQDHGTSLTCQVTLPGAGVTMTRAVRLNISY
   597 AA.
   EMBL; AF293372; AAL09302.1; -
   STANDARD;
  ELHYATLNFP 488
  585 GYEYSEINIP 594
  NCBI_TaxID=9598;
   Name=SIGLECL1;
   SILL PANTR
Q95LH0;
  127
   256
  364
   307
  478
   535
  187
   RESULT 11
SILL PANTR
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way incofitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   99
   N-linked (Glonac. ) (Potential).
N-linked (Glonac. ) (Potential).
N-linked (Glonac. ) (Potential).
N-linked (Glonac. ) (Potential).
LLLLIPPLLCGRVGAKEQKDYLLTMQKSVTVQEGLCVSVLC
   SFSYPQNGWTASDPVHGYWFRAGDHVSRNI PVATNNPARAV
  <u> OEETRDRPHLLGDPQNKDCTLSIRDTRESDAGTYVFCVERG</u>
  7 LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE
  67 ITKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYV
   Sialic acid binding Ig-like lectin-like
  NMKWNYKYDOLSVNV -> PLLWANEERDSGGWADPRFS
  (Potential). (Potential). (Potential).
(sialic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
  Pfan; PF00047; ig; 4.

PROSITE, PS50835; IG LIKE; 3.
Alternative splicting; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
  Length 595;
   174; Indels
   Cytoplasmic (Potential).

[19-like V-type 1.
[19-like V-type 2.
[19-like C2-type 2.
[19-like C2-type 2.
[1]-like C2-type 2.
[1]-like C2-type 2.
[2]-like C2-type 2.
[3]-like C2-type 3.
[4]-like MOTIF.
[5]-like MOTIF.
[6]-like MOTIF.
[7]-like MOTIF.
[8]-like MOTIF.
[8]-like MOTIF.
[8]-like MOTIF.
[8]-like MOTIF.
[9]-like MOTIF.
[9]-li
   Extracellular (Potential).
  TIG=VSP 002566.
-> T (in dbSNP:2034891).
TIG=VAR 014259.
-> W (in Ref. 3).
  D05662176274C5C3 CRC64;
  33.6%; Score 909; DB 1;
llarity 43.1%; Pred. No. 1.4e-53;
Conservative 65; Mismatches 174;
  isoform Short)
   Potential
   /FTId=VSP
   /FTId=VAR
  EMBL, AF277806, AAK51233.1, -.
EMBL, AF277806, AAK51234.1, -
EMBL, AF282256, AAK71521.1, -.
EMBL, AY356140, AAQ88507.1, -.
EMBL, BC035809, AAH35809.2, -.
  64984 MW;
   InterPro; IPR007110; Ig-like.
  HGNC:15482; SIGLECL1.
   81
  EMBL, BC035809; AAH31
HSSP, Q9Y286; 1075.
Genew; HGNC:15482; S1
MIM; 606094; -
   528 5
595 AA;
  Local Similarity
es 211; Conserv
   19
   Transmembrane.
  Query Match
Best Local S
Matches 211
  DOMAIN
TRANSMEM
DOMAIN
   DOMAIN
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DOMAIN
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SITE
SITE
DISULFID
   DISULFID
   CONFLICT
  137
  DISULFID
  CARBOHYD
   CARBOHYD
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   VARSPLIC
   VARIANT
   SIGNAL
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